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- (54) **SYNTHETIC PROMOTER AND METHODS OF USE THEREOF**
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(58) **Field of Classification Search**  
None  
See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to methods for the design and production of synthetic promoters with a defined specificity and promoters produced with these methods.

**9 Claims, 3 Drawing Sheets**  
**Specification includes a Sequence Listing.**

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### p-BnArc5 perm in canola

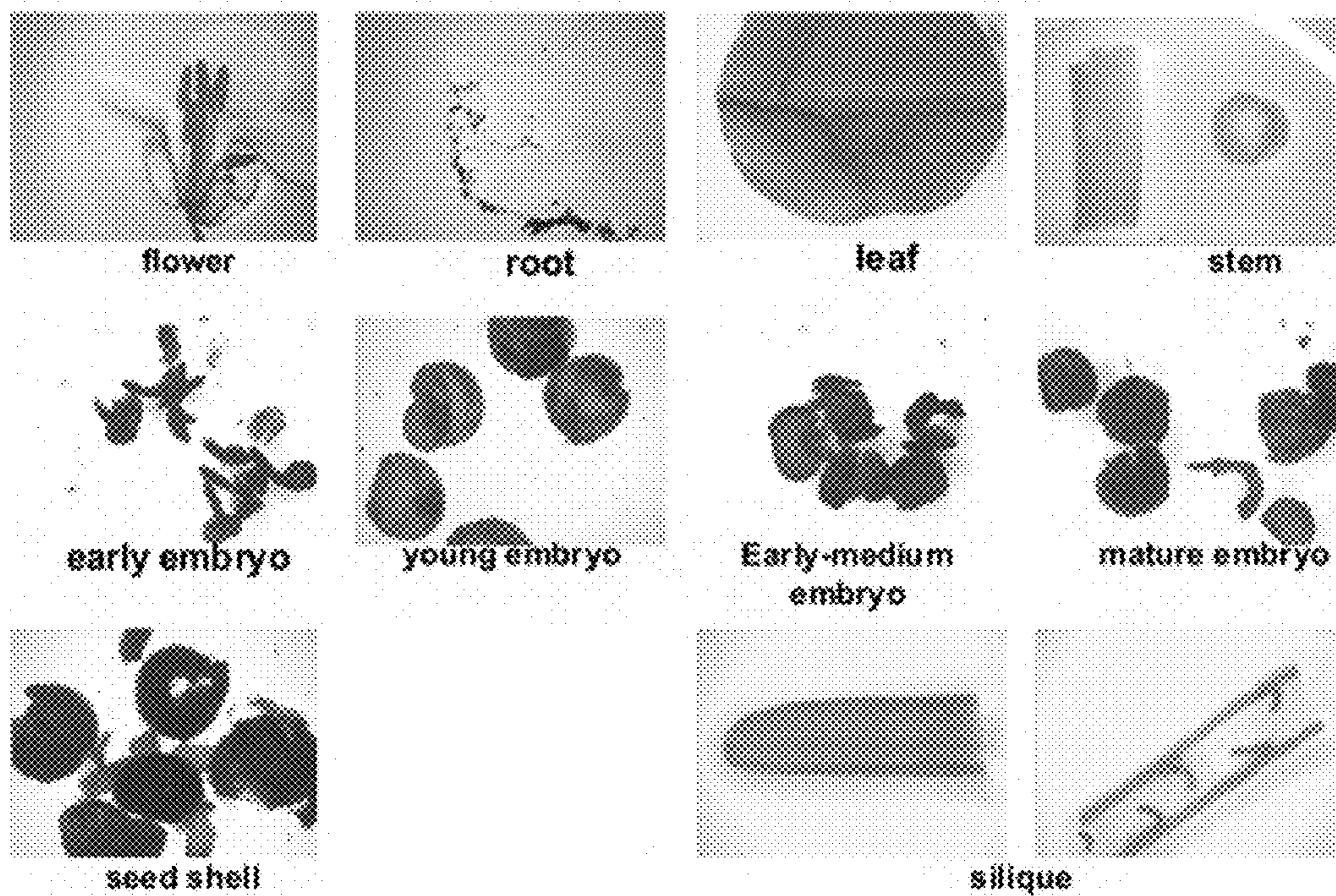


FIGURE 1

### p-VfSBP perm in canola

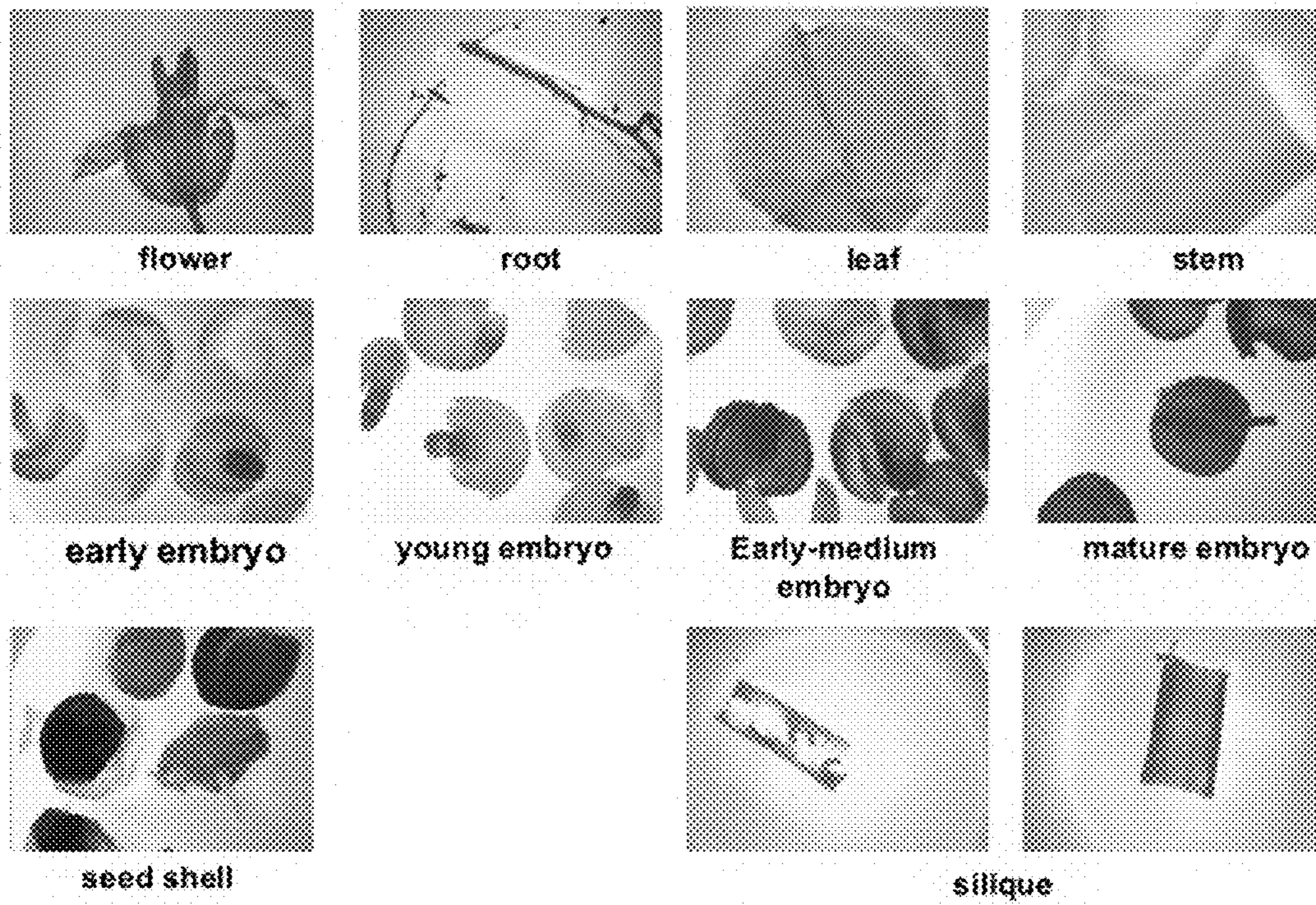


FIGURE 2

### pBnNapin perm in Arabidopsis

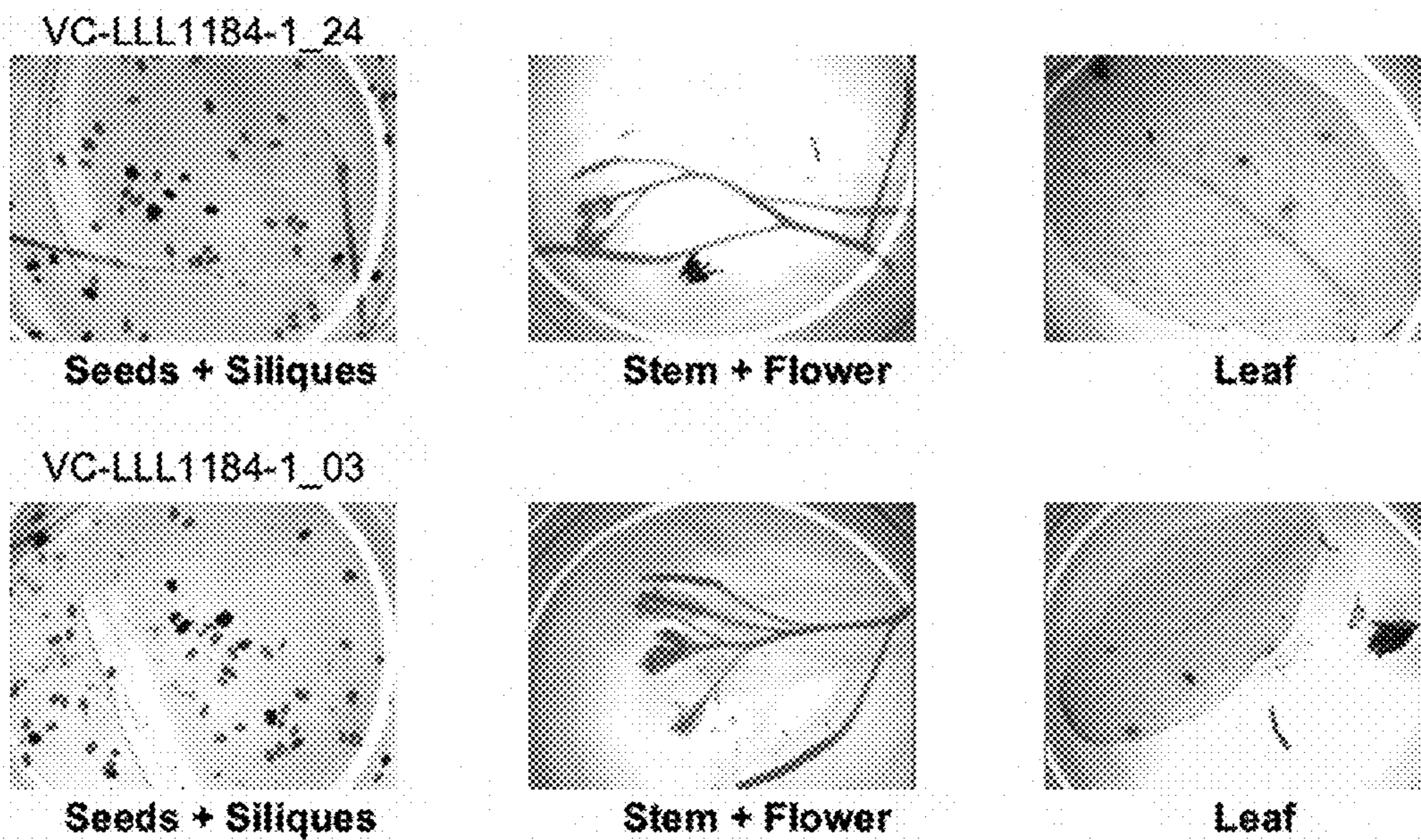


FIGURE 3

## SYNTHETIC PROMOTER AND METHODS OF USE THEREOF

This Application is a continuation of U.S. application Ser. No. 13/991,566, which is a U.S. National Stage Application of PCT/IB2011/055412, filed Dec. 1, 2011, which claims the benefit of U.S. Provisional Application No. 61/419,895, filed Dec. 6, 2010, and which also claims priority under 35 U.S.C. § 119 to European Patent Application No. 10193800.9, filed Dec. 6, 2010; the entire contents of these applications are hereby incorporated by reference herein in their entirety.

### INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

The Sequence Listing, which is a part of the present disclosure, is submitted concurrently with the specification as a text file. The name of the text file containing the Sequence Listing is "70392A\_Seqlisting.txt", which was created on Nov. 7, 2017 and is 99,055 bytes in size. The subject matter of the Sequence Listing is incorporated herein in its entirety by reference.

### FIELD OF THE INVENTION

The present invention relates to methods for the design and production of synthetic promoters with a defined specificity and promoters produced with these methods.

### BACKGROUND OF THE INVENTION

Manipulation of plants to alter and/or improve phenotypic characteristics such as productivity or quality requires expression of heterologous genes in plant tissues. Such genetic manipulation relies on the availability of a means to drive and to control gene expression as required. For example, genetic manipulation relies on the availability and use of suitable promoters which are effective in plants and which regulate gene expression so as to give the desired effect(s) in the transgenic plant.

Advanced traits often require the coordinated expression of more than one gene in a transgenic plant. For example, to achieve the production of polyunsaturated fatty acids such as archachidonic acid in a plant requires expression of at least 5 genes. There is also increasing demand of trait stacking which requires the combination of more than one gene in transgenic plants.

The availability of suitable promoters for such coordinated expression is limited. Promoters would often need to have the same tissue and/or developmental specificity and preferably comparable expression strength. One solution has been to use the same promoter for the expression of several genes. Expression constructs comprising more than one expression cassette with tandem or inverted sequence repeats of for example a promoter cause various problems. When located on one vector, handling of the vector in bacteria for cloning, amplification and transformation is difficult due to recombination events which lead to the loss and/or rearrangement of part of the expression construct. Moreover, sequence verification of constructs comprising repeated sequences is difficult and sometimes impossible. A further problem of such expression constructs comprising repeats of the same promoter sequence is that recombination may also occur after introduction into the genome of the target organism such as a plant.

Additionally it is well known that repeated promoter sequences in the genome of organisms such as a plant may

induce silencing of expression derived from these promoters, for example by methylation of the promoter or increase of chromatin density at the site of the promoters which makes the promoter inaccessible for transcription factors.

The use of different promoters in expression constructs comprising more than one expression cassette is one possibility to circumvent these problems. Isolation and analysis of promoters is laborious and time consuming. It is unpredictable what expression pattern and expression strength an isolated promoter will have and hence a high number of promoters need to be tested in order to find at least two promoters with comparable expression pattern and optionally comparable expression strength.

There is, therefore, a great need in the art for the availability of new sequences that may be used for expression of selected transgenes in economically important plants. It is thus an objective of the present invention to provide new methods for the production of synthetic promoters with identical and/or overlapping expression pattern or expression specificity and optionally similar expression strength. This objective is solved by the present invention.

### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the gene expression activity conferred by p-PvArc5\_perm as described in Example 2.

FIG. 2 shows the gene expression activity conferred by p-VfSBP\_perm as described in Example 2.

FIG. 3 shows gene expression activity conferred by pBn-Napin and p-BNnapin\_perm as described in Example 4.

### DETAILED DESCRIPTION OF THE INVENTION

A first embodiment of the invention is a method for the production of one or more synthetic regulatory nucleic acid molecules of a defined specificity comprising the steps of

- a) identifying at least one naturally occurring nucleic acid molecule of the defined specificity (starting molecule) and
- b) identifying conserved motives in the at least one nucleic acid sequence (starting sequence) of the starting molecule of the defined specificity as defined in a) and
- c) mutating the starting sequence while
  - i) leaving at least 70%, preferably 80%, 85%, 90%, more preferably at least 95%, even more preferably at least 98% or at least 99% for example 100% of the motives unaltered known to be involved in regulation of the respective defined specificity (also called preferentially associated motives) and
  - ii) leaving at least 80%, preferably at least 90%, 95% for example 100% of the motives unaltered involved in transcription initiation (also called essential motives) and
  - iii) leaving at least 10%, preferably at least 20%, 30%, 40% or 50%, more preferably at least 60%, 70% or 80%, even more preferably at least 90% or 95% of other identified motives (also called non exclusively associated) unaltered and
  - iv) keeping the arrangement of the identified motives substantially unchanged and
  - v) avoiding the introduction of new motives known to influence expression with another specificity than said defined specificity and
  - vi) avoiding identical stretches of more than 50 basepairs, preferably 45 basepairs, more preferably 40 basepairs, most preferably 35 basepairs, for example 30 basepairs

- between each of the starting sequence and the one or more mutated sequences and
- d) producing a nucleic acid molecule comprising the mutated sequence and
  - e) optionally testing the specificity of the mutated sequence in the respective organism.

In one embodiment of the invention, additional preferably associated motives may be introduced into the sequence of the synthetic nucleic acid molecule.

Production of the nucleic acid molecule comprising the mutated sequence could for example be done by chemical synthesis or by oligo ligation whereby smaller oligos comprising parts of the sequence of the invention are stepwise annealed and ligated to form the nucleic acid molecule of the invention.

In a preferred embodiment of the invention, the synthetic regulatory nucleic acid molecule is a synthetic promoter, in a more preferred embodiment the synthetic regulatory nucleic acid molecule is a synthetic promoter functional in a plant, plant tissue or plant cell.

The at least one starting molecule comprising the starting sequence may for example be identified by searches in literature or internet resources such as sequence and/or gene expression data bases. The at least one starting molecule comprising the starting sequence may in another example be identified by isolation and characterization of a natural occurring promoter from the respective organism, for example plants, algae, fungi, animals and the like. Such methods are well known to a person skilled in the art and for example described in Back et al., 1991, Keddie et al., 1992, Keddie et al., 1994.

Motives in a series of nucleic acid molecules may be identified by a variety of bioinformatic tools available in the art. For example see Hehl and Wingender, 2001, Hehl and Bulow, 2002, Cartharius et al., 2005, Kaplan et al., 2006, Dare et al., 2008.

In addition, there are various databases available specialized in promoter analysis and motif prediction in any given sequence. For example as reviewed in Hehl and Wingender, 2001.

It is also possible to identify motives necessary for regulation of expression of the defined specificity with experimental methods known to a skilled person. Such methods are for example deletion or mutation analysis of the respective starting sequence as for example described in Montgomery et al., 1993.

Essential motives known to be involved in transcription initiation for example by being bound by general initiation factors and/or RNA polymerases as described above under ii) are for example the TATA box, the CCAAT box, the GC box or other functional similar motives as for example identified in Roeder (1996, Trends in Biochemical Science, 21(9)) or Baek et al. (2006, Journal of Biological Chemistry, 281). These motives allow a certain degree of degeneration or variation of their sequence without changing or destroying their functionality in initiation of transcription. The skilled person is aware of such sequence variations that leave the respective motives functional. Such variations are for example given in the Transfac database as described by Matys et al, ((2003) NAR 31 (1)) and literature given therein. The Transfac database may for example be accessed via <ftp://ftp.ebi.ac.uk/pub/databases/transfac/transfac32.tar.Z>. Hence it is to be understood that the term

“leaving motives unaltered involved in transcription initiation” means that the respective motives may be mutated, hence altered in their sequence as long as their respective function which is enabling initiation of transcription is not

altered, hence as long as the essential motives are functional. In another embodiment of the invention the first 49, preferably 44, more preferably 39, even more preferably 34, most preferably 29 bp directly upstream of the transcription initiation site are kept unaltered.

The term “keeping the arrangement of the motives unchanged” as used above under iv) means, that the order of the motives and/or the distance between the motives are kept substantially unchanged, preferably unchanged. Substantially unchanged means, that the distance between two motives in the starting sequence does not differ from the distance between these motives in the synthetic regulatory nucleic acid sequence, hence the distance between said motives is not longer or shorter, by more than 100%, for example 90%, 80% or 70%, preferably 60%, 50% or 40%, more preferably not more than 30% or 20%, most preferably not more than 10% in the synthetic regulatory nucleic acid sequence as compared to the starting sequence. Preferably the distance between two motives in the starting sequence differs by not more than 10, preferably 9, more preferably 8 or 7 or 6 or 5 or 4, even more preferably not more than 3 or 2, most preferably not more than 1 basepairs from the distance in the permuted sequence.

Inverted and/or direct stretches of repeated sequences may lead to the formation of secondary structures in plasmids or genomic DNA. Repeated sequences may lead to recombination, deletion and/or rearrangement in the plasmid both in *E. coli* and *Agrobacterium*. In eukaryotic organisms, for example plants, repeated sequences also tend to be silenced by methylation. Recombination events which lead to deletions or rearrangements of one or more expression cassettes and/or T-DNAs are likely to lead to loss of function for example loss of expression of such constructs in the transgenic plant (Que and Jorgensen, 1998, Hamilton et al., 1998). It is therefore a critical feature of the invention at hand to avoid identical stretches of 50 basepairs, preferably 45 basepairs, more preferably 40 basepairs, most preferably 35 basepairs, for example 30 basepairs between each of the starting sequence and the one or more permuted sequences. In case of the production of more than one permuted sequences said identical stretches must be avoided between the starting sequence and each of the permuted sequences in a pair wise comparison. In another embodiment, such identical stretches must be avoided between all permuted sequences and the starting sequence; hence none of the permuted and starting sequences shares such identical stretches with any of the other sequences.

The skilled person is aware that regulatory nucleic acids may comprise promoters and functionally linked to said promoters 5'UTR the latter may comprise at least one intron. It has been shown, that introns may be lead to increased expression levels derived from the promoter to which the 5'UTR comprising the intron is functionally linked. The 5' UTR and the intron may be altered in their sequence as described, wherein the splice sites and putative branching point are not altered in order to ensure correct splicing of the intron after permutation. No nucleotide exchanges are introduced into sequences at least 2, preferably at least 3, more preferably at least 5, even more preferably at least 10 bases up- and downstream of the splice sites (5' GT; 3' CAG) are kept unchanged. In addition, “CURAY” and “TNA” sequence elements being potential branching points of the intron are kept unchanged within the last 200 base pairs, preferably the last 150 base pairs, more preferably the last 100 base pairs, even more preferably the last 75 base pairs of the respective intron.

## 5

The 5'UTR may be permuted according to the rules as defined above, wherein preferably at least 25, more preferably at least 20, even more preferably at least 15, for example at least 10, most preferably at least 5 base pairs up and downstream of the transcription start are kept unchanged. The AT content of both the 5' UTR and the intron is not changed by more than 20%, preferably not more than 15%, for example 10% or 5% compared to the AT content of the starting sequence.

A further embodiment of the invention is a synthetic regulatory nucleic acid molecule produced according to the method of the invention.

An expression construct comprising the said synthetic regulatory nucleic acid molecule is another embodiment of the invention.

A vector comprising the regulatory nucleic acid molecule or the expression construct of the invention is also comprised in this invention, as well as microorganisms, plant cells or animal cells comprising the regulatory nucleic acid molecule, the expression construct and/or the vector of the invention.

A further embodiment of the invention is a plant, plant seed, plant cell or part of a plant comprising the regulatory nucleic acid molecule, the expression construct and/or the vector of the invention.

A further embodiment of the invention are exemplary recombinant seed specific or seed preferential synthetic regulatory nucleic acid molecules produced according to the method of the invention wherein the regulatory nucleic acid molecule is comprised in the group consisting of

I) a nucleic acid molecule represented by SEQ ID NO: 2, 4 or 6 and

II) a nucleic acid molecule comprising at least 1000 consecutive base pairs, for example 1000 base pairs, preferably at least 800 consecutive base pairs, for example 800 base pairs, more preferably at least 700 consecutive base pairs, for example 700 base pairs, even more preferably at least 600 consecutive base pairs, for example 600 base pairs, most preferably at least 500 consecutive base pairs, for example 500 base pairs or at least 400, at least 300, at least 250 for example 400, 300 or 250 base pairs of a sequence described by SEQ ID NO: 2, 4 or 6 and

III) a nucleic acid molecule having an identity of at least 70%, for example at least 75%, 76%, 77%, 78%, 79% preferably at least 80%, for example at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, more preferably 90%, for example at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, even more preferably 98% most preferably 99% over a sequence of at least 250, 300, 400, 500, 600 preferably 700, more preferably 800, even more preferably 900, most preferably 1000 consecutive nucleic acid base pairs to a sequences described by SEQ ID NO: 2, 4 or 6 and

IV) a nucleic acid molecule having an identity of at least 70%, for example at least 75%, 76%, 77%, 78%, 79% preferably at least 80%, for example at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, more preferably 90%, for example at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, even more preferably 98% most preferably 99% to a sequence consisting of at least 50%, 60%, 70%, 80%, 90% or 100% of any of the sequences described by SEQ ID NO: 2, 4 or 6 and

V) a nucleic acid molecule hybridizing under high stringent, preferably very high stringent conditions with a nucleic acid molecule of at least 250, 300, 400, 500, 600, 700, 800, 900, 1000 or the complete consecutive

## 6

base pairs of a nucleic acid molecule described by any of SEQ ID NO: 2, 4 or 6 and

VI) a complement of any of the nucleic acid molecules as defined in I) to V).

Another embodiment of the invention are exemplary recombinant seed specific or seed preferential synthetic regulatory nucleic acid molecules produced according to the method of the invention wherein the regulatory nucleic acid molecule is comprised in the group consisting of

i) a nucleic acid molecule represented by SEQ ID NO: 2, 4 or 6 and

ii) a nucleic acid molecule comprising at least 1000 consecutive base pairs, for example 1000 base pairs, preferably at least 800 consecutive base pairs, for example 800 base pairs, more preferably at least 700 consecutive base pairs, for example 700 base pairs, even more preferably at least 600 consecutive base pairs, for example 600 base pairs, most preferably at least 500 consecutive base pairs, for example 500 base pairs or at least 400, at least 300, at least 250 for example 400, 300 or 250 base pairs of a sequence described by SEQ ID NO: 2, 4 or 6 and

iii) a nucleic acid molecule having an identity of at least 75% over a sequence of at least 250, 300, 400, 500, 600 preferably 700, more preferably 800, even more preferably 900, most preferably 1000 or the complete consecutive nucleic acid base pairs to a sequences described by SEQ ID NO: 6,

iv) a nucleic acid molecule having an identity of at least 90% over a sequence of at least 250, 300, 400, 500, 600 preferably 700, more preferably 800, even more preferably 900, most preferably 1000 or the complete consecutive nucleic acid base pairs to a sequences described by SEQ ID NO: 2 or 4 and

v) a nucleic acid molecule hybridizing under high stringent, preferably very high stringent conditions with a nucleic acid molecule of at least 250, 300, 400, 500, 600, 700, 800, 900, 1000 or the complete consecutive base pairs of a nucleic acid molecule described by any of SEQ ID NO: 2, 4 or 6 and

vi) a complement of any of the nucleic acid molecules as defined in i) to v).

Further embodiments of the invention are exemplary recombinant constitutive regulatory nucleic acid molecules produced according to the method of the invention wherein the regulatory nucleic acid molecule is comprised in the group consisting of

I) a nucleic acid molecule represented by SEQ ID NO: 14 or 15 and

II) a nucleic acid molecule comprising at least 1750, 1500, 1250 or 1000 consecutive base pairs, for example 1000 base pairs, preferably at least 800 consecutive base pairs, for example 800 base pairs, more preferably at least 700 consecutive base pairs, for example 700 base pairs, even more preferably at least 600 consecutive base pairs, for example 600 base pairs, most preferably at least 500 consecutive base pairs, for example 500 base pairs or at least 400, at least 300, at least 250 for example 400, 300 or 250 base pairs of a sequence described by SEQ ID NO: 14 or 15 and

III) a nucleic acid molecule having an identity of at least 70%, for example at least 75%, 76%, 77%, 78%, 79% preferably at least 80%, for example at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, more preferably 90%, for example at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, even more preferably 98% most preferably 99% over a sequence of at least 250, 300,



400, 500, 600 preferably 700, more preferably 800, even more preferably 900, for example 1000, most preferably 1250, for example 1500 or 1750 or 2000 consecutive nucleic acid base pairs to a sequences described by SEQ ID NO: 14 or 15 and

IV) a nucleic acid molecule having an identity of at least 70%, for example at least 75%, 76%, 77%, 78%, 79% preferably at least 80%, for example at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, more preferably 90%, for example at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, even more preferably 98% most preferably 99% to a sequence consisting of at least 50%, 60%, 70%, 80%, 90% or 100% of any of the sequences described by SEQ ID NO: 14 or 15 and

V) a nucleic acid molecule hybridizing under high stringent, preferably very high stringent conditions with a nucleic acid molecule of at least 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1250, 1500, 1750 or 2000 or the complete consecutive base pairs of a nucleic acid molecule described by any of SEQ ID NO: 14 or 15 and

VI) a complement of any of the nucleic acid molecules as defined in I) to V).

Another embodiment of the invention are exemplary recombinant constitutive synthetic regulatory nucleic acid molecules produced according to the method of the invention wherein the regulatory nucleic acid molecule is comprised in the group consisting of

i) a nucleic acid molecule represented by SEQ ID NO: 14 or 15 and

ii) a nucleic acid molecule comprising at least 2000, 1750, 1500, 1250 or 1000 consecutive base pairs, for example 1000 base pairs, preferably at least 800 consecutive base pairs, for example 800 base pairs, more preferably at least 700 consecutive base pairs, for example 700 base pairs, even more preferably at least 600 consecutive base pairs, for example 600 base pairs, most preferably at least 500 consecutive base pairs, for example 500 base pairs or at least 400, at least 300, at least 250 for example 400, 300 or 250 base pairs of a sequence described by SEQ ID NO: 14 or 15 and

iii) a nucleic acid molecule having an identity of at least 95%, preferably 97%, more preferably 98%, most preferably 99% over a sequence of at least 250, 300, 400, 500, 600 preferably 700, more preferably 800, even more preferably 900, fore example 1000, most preferably 1500, for example 2000 or the complete consecutive nucleic acid base pairs to a sequences described by SEQ ID NO: 14 or 15,

iv) a nucleic acid molecule hybridizing under high stringent, preferably very high stringent conditions with a nucleic acid molecule of at least 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1250. 1500, 1750, 2000 or the complete consecutive base pairs of a nucleic acid molecule described by any of SEQ ID NO: 14 or 15 and

v) a complement of any of the nucleic acid molecules as defined in i) to v).

It is to be understood, that the group of exemplary recombinant seed specific or seed preferential or constitutive synthetic regulatory nucleic acid molecules produced according to the method of the invention as defined above under I) to V) and i) to vi) does not comprise the starting molecules as defined by SEQ ID NO: 1, 3, 5 and 13 or a complement thereof or a nucleic acid molecule having at least 250 consecutive base pairs of a sequence described by

SEQ ID NO: 1, 3, 5 or 13 or a complement thereof or any other nucleic acid molecule occurring in a wild type plant as

such nucleic acid molecules are molecules that are not produced according to the invention but are naturally present in wild type plants.

An expression construct comprising any of said synthetic regulatory nucleic acid molecules as defined above under I) to VI) and i) to vi) is another embodiment of the invention.

A vector comprising the regulatory nucleic acid molecule or the expression construct of the invention is also comprised in this invention, as well as microorganisms, plant cells or animal cells comprising the regulatory nucleic acid molecule, the expression construct and/or the vector of the invention.

A further embodiment of the invention is a plant, plant seed, plant cell or part of a plant comprising the regulatory nucleic acid molecule, the expression construct and/or the vector of the invention.

### Definitions

Abbreviations: GFP—green fluorescence protein, GUS—beta-Glucuronidase, BAP—6-benzylaminopurine; 2,4-D—2,4-dichlorophenoxyacetic acid; MS—Murashige and Skoog medium; NAA—1-naphtaleneacetic acid; MES, 2-(N-morpholino-ethanesulfonic acid, IAA indole acetic acid; Kan: Kanamycin sulfate; GA3—Gibberellic acid; Timentin™: ticarcillin disodium/clavulanate potassium.

It is to be understood that this invention is not limited to the particular methodology or protocols. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims. It must be noted that as used herein and in the appended claims, the singular forms “a,” “and,” and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to “a vector” is a reference to one or more vectors and includes equivalents thereof known to those skilled in the art, and so forth. The term “about” is used herein to mean approximately, roughly, around, or in the region of. When the term “about” is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term “about” is used herein to modify a numerical value above and below the stated value by a variance of 20 percent, preferably 10 percent up or down (higher or lower). As used herein, the word “or” means any one member of a particular list and also includes any combination of members of that list. The words “comprise,” “comprising,” “include,” “including,” and “includes” when used in this specification and in the following claims are intended to specify the presence of one or more stated features, integers, components, or steps, but they do not preclude the presence or addition of one or more other features, integers, components, steps, or groups thereof. For clarity, certain terms used in the specification are defined and used as follows:

Antiparallel: “Antiparallel” refers herein to two nucleotide sequences paired through hydrogen bonds between complementary base residues with phosphodiester bonds running in the 5'-3' direction in one nucleotide sequence and in the 3'-5' direction in the other nucleotide sequence.

Antisense: The term “antisense” refers to a nucleotide sequence that is inverted relative to its normal orientation for transcription or function and so expresses an RNA transcript that is complementary to a target gene mRNA molecule expressed within the host cell (e.g., it can hybridize to the target gene mRNA molecule or single stranded genomic

DNA through Watson-Crick base pairing) or that is complementary to a target DNA molecule such as, for example genomic DNA present in the host cell.

“Box” or as synonymously used herein “motif” or “cis-element” of a promoter means a transcription factor binding sequence defined by a highly conserved core sequence of approximately 4 to 6 nucleotides surrounded by a conserved matrix sequence of in total up to 20 nucleotides within the plus or minus strand of the promoter, which is able of interacting with the DNA binding domain of a transcription factor protein. The conserved matrix sequence allows some variability in the sequence without losing its ability to be bound by the DNA binding domain of a transcription factor protein.

One way to describe transcription factor binding sites (TFBS) is by nucleotide or position weight matrices (NWM or PWM) (for review see Stormo, 2000). A weight matrix pattern definition is superior to a simple IUPAC consensus sequence as it represents the complete nucleotide distribution for each single position. It also allows the quantification of the similarity between the weight matrix and a potential TFBS detected in the sequence (Cartharius et al. 2005).

Coding region: As used herein the term “coding region” when used in reference to a structural gene refers to the nucleotide sequences which encode the amino acids found in the nascent polypeptide as a result of translation of a mRNA molecule. The coding region is bounded, in eukaryotes, on the 5'-side by the nucleotide triplet “ATG” which encodes the initiator methionine and on the 3'-side by one of the three triplets which specify stop codons (i.e., TAA, TAG, TGA). In addition to containing introns, genomic forms of a gene may also include sequences located on both the 5'- and 3'-end of the sequences which are present on the RNA transcript. These sequences are referred to as “flanking” sequences or regions (these flanking sequences are located 5' or 3' to the non-translated sequences present on the mRNA transcript). The 5'-flanking region may contain regulatory sequences such as promoters and enhancers which control or influence the transcription of the gene. The 3'-flanking region may contain sequences which direct the termination of transcription, post-transcriptional cleavage and polyadenylation.

Complementary: “Complementary” or “complementarity” refers to two nucleotide sequences which comprise antiparallel nucleotide sequences capable of pairing with one another (by the base-pairing rules) upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences. For example, the sequence 5'-AGT-3' is complementary to the sequence 5'-ACT-3'. Complementarity can be “partial” or “total.” “Partial” complementarity is where one or more nucleic acid bases are not matched according to the base pairing rules. “Total” or “complete” complementarity between nucleic acid molecules is where each and every nucleic acid base is matched with another base under the base pairing rules. The degree of complementarity between nucleic acid molecule strands has significant effects on the efficiency and strength of hybridization between nucleic acid molecule strands. A “complement” of a nucleic acid sequence as used herein refers to a nucleotide sequence whose nucleic acid molecules show total complementarity to the nucleic acid molecules of the nucleic acid sequence.

Conserved motives: A conserved motif as used herein means a sequence motif or box found in various promoters having the same or overlapping specificity. Overlapping specificity means the specificity of at least two promoters wherein the expression derived from one promoter is in part

or completely in the same for example tissue as the other promoter, wherein the latter one may drive expression in additional tissues in which the first promoter may not drive expression. Motives may be grouped in three classes:

5 Essential: motives present in the promoters of most genes that are transcribed by RNA Polymerase II and which are preferentially localized close to the transcription start side. Such motives must not be made dysfunctional by mutations according to the method of the invention. Hence they must not be altered in a way that prevents them from being bound by the respective DNA binding domain of the transcription factor protein that would have bound to the unaltered sequence.

10 non exclusively associated: motives present in the promoters of genes that are associated with certain tissues/physiological states/treatments but not exclusively, they may be expressed also in other tissues/physiological states/treatments. According to the method of the invention, such motives should preferably not be made dysfunctional by mutations or at least only a certain percentage of such motives present in one particular promoter or starting sequence. Hence they should preferably not be altered in a way that prevents them from being bound by the respective DNA binding domain of the transcription factor protein that would have bound to the unaltered sequence.

15 preferentially associated: motives present in the promoters of genes that are expressed preferentially in specific tissues/physiological states/treatments. The vast majority of such motives identified in a starting sequence must not be made dysfunctional by mutations according to the method of the invention. Hence they must not be altered in a way that prevents them from being bound by the respective DNA binding domain of the transcription factor protein that would have bound to the unaltered sequence.

20 Defined specificity: the term “defined specificity” means any expression specificity of a promoter, preferably a plant specific promoter, which is beneficial for the expression of a distinct coding sequence or RNA. A defined specificity may for example be a tissue or developmental specificity or the expression specificity could be defined by induction or repression of expression by biotic or abiotic stimuli or a combination of any of these.

25 Double-stranded RNA: A “double-stranded RNA” molecule or “dsRNA” molecule comprises a sense RNA fragment of a nucleotide sequence and an antisense RNA fragment of the nucleotide sequence, which both comprise nucleotide sequences complementary to one another, thereby allowing the sense and antisense RNA fragments to pair and form a double-stranded RNA molecule.

30 Endogenous: An “endogenous” nucleotide sequence refers to a nucleotide sequence, which is present in the genome of the untransformed plant cell.

35 Expression: “Expression” refers to the biosynthesis of a gene product, preferably to the transcription and/or translation of a nucleotide sequence, for example an endogenous gene or a heterologous gene, in a cell. For example, in the case of a structural gene, expression involves transcription of the structural gene into mRNA and—optionally—the subsequent translation of mRNA into one or more polypeptides. In other cases, expression may refer only to the transcription of the DNA harboring an RNA molecule. Expression may also refer to the change of the steady state level of the respective RNA in a plant or part thereof due to change of the stability of the respective RNA.

40 Similar expression strength: Two or more regulatory nucleic acid molecules have a similar expression strength when the expression derived from any of the regulatory

nucleic acid molecule in a distinct cell, tissue or plant organ does not deviate by more than factor 2.

Expression construct: "Expression construct" as used herein mean a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate part of a plant or plant cell, comprising a promoter functional in said part of a plant or plant cell into which it will be introduced, operatively linked to the nucleotide sequence of interest which is—optionally—operatively linked to termination signals. If translation is required, it also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region may code for a protein of interest but may also code for a functional RNA of interest, for example RNAa, siRNA, snoRNA, snRNA, microRNA, ta-siRNA or any other noncoding regulatory RNA, in the sense or antisense direction. The expression construct comprising the nucleotide sequence of interest may be chimeric, meaning that one or more of its components is heterologous with respect to one or more of its other components. The expression construct may also be one, which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression construct is heterologous with respect to the host, i.e., the particular DNA sequence of the expression construct does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression construct may be under the control of a constitutive promoter or of an inducible promoter, which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a plant, the promoter can also be specific to a particular tissue or organ or stage of development.

Expression pattern or expression specificity of a regulatory nucleic acid molecule as used herein defines the tissue and/or developmental and/or environmentally modulated expression of a coding sequence or RNA under the control of a distinct regulatory nucleic acid molecule.

Foreign: The term "foreign" refers to any nucleic acid molecule (e.g., gene sequence) which is introduced into the genome of a cell by experimental manipulations and may include sequences found in that cell so long as the introduced sequence contains some modification (e.g., a point mutation, the presence of a selectable marker gene, etc.) and is therefore distinct relative to the naturally-occurring sequence.

Functional linkage: The term "functional linkage" or "functionally linked" is to be understood as meaning, for example, the sequential arrangement of a regulatory element (e.g. a promoter) with a nucleic acid sequence to be expressed and, if appropriate, further regulatory elements (such as e.g., a terminator or an enhancer) in such a way that each of the regulatory elements can fulfill its intended function to allow, modify, facilitate or otherwise influence expression of said nucleic acid sequence. As a synonym the wording "operable linkage" or "operably linked" may be used. The expression may result depending on the arrangement of the nucleic acid sequences in relation to sense or antisense RNA. To this end, direct linkage in the chemical sense is not necessarily required. Genetic control sequences such as, for example, enhancer sequences, can also exert their function on the target sequence from positions which are further away, or indeed from other DNA molecules. Preferred arrangements are those in which the nucleic acid sequence to be expressed recombinantly is positioned behind the sequence acting as promoter, so that the two

sequences are linked covalently to each other. The distance between the promoter sequence and the nucleic acid sequence to be expressed recombinantly is preferably less than 200 base pairs, especially preferably less than 100 base pairs, very especially preferably less than 50 base pairs. In a preferred embodiment, the nucleic acid sequence to be transcribed is located behind the promoter in such a way that the transcription start is identical with the desired beginning of the chimeric RNA of the invention. Functional linkage, and an expression construct, can be generated by means of customary recombination and cloning techniques as described (e.g., in Maniatis T, Fritsch E F and Sambrook J (1989) *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor (N.Y.); Silhavy et al. (1984) *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor (N.Y.); Ausubel et al. (1987) *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and Wiley Interscience; Gelvin et al. (Eds) (1990) *Plant Molecular Biology Manual*; Kluwer Academic Publisher, Dordrecht, The Netherlands). However, further sequences, which, for example, act as a linker with specific cleavage sites for restriction enzymes, or as a signal peptide, may also be positioned between the two sequences. The insertion of sequences may also lead to the expression of fusion proteins. Preferably, the expression construct, consisting of a linkage of a regulatory region for example a promoter and nucleic acid sequence to be expressed, can exist in a vector-integrated form and be inserted into a plant genome, for example by transformation.

Gene: The term "gene" refers to a region operably joined to appropriate regulatory sequences capable of regulating the expression of the gene product (e.g., a polypeptide or a functional RNA) in some manner. A gene includes untranslated regulatory regions of DNA (e.g., promoters, enhancers, repressors, etc.) preceding (up-stream) and following (downstream) the coding region (open reading frame, ORF) as well as, where applicable, intervening sequences (i.e., introns) between individual coding regions (i.e., exons). The term "structural gene" as used herein is intended to mean a DNA sequence that is transcribed into mRNA which is then translated into a sequence of amino acids characteristic of a specific polypeptide.

Genome and genomic DNA: The terms "genome" or "genomic DNA" is referring to the heritable genetic information of a host organism. Said genomic DNA comprises the DNA of the nucleus (also referred to as chromosomal DNA) but also the DNA of the plastids (e.g., chloroplasts) and other cellular organelles (e.g., mitochondria). Preferably the terms genome or genomic DNA is referring to the chromosomal DNA of the nucleus.

Heterologous: The term "heterologous" with respect to a nucleic acid molecule or DNA refers to a nucleic acid molecule which is operably linked to, or is manipulated to become operably linked to, a second nucleic acid molecule to which it is not operably linked in nature, or to which it is operably linked at a different location in nature. A heterologous expression construct comprising a nucleic acid molecule and one or more regulatory nucleic acid molecule (such as a promoter or a transcription termination signal) linked thereto for example is a constructs originating by experimental manipulations in which either a) said nucleic acid molecule, or b) said regulatory nucleic acid molecule or c) both (i.e. (a) and (b)) is not located in its natural (native) genetic environment or has been modified by experimental manipulations, an example of a modification being a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. Natural genetic environment

refers to the natural chromosomal locus in the organism of origin, or to the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the sequence of the nucleic acid molecule is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least at one side and has a sequence of at least 50 bp, preferably at least 500 bp, especially preferably at least 1,000 bp, very especially preferably at least 5,000 bp, in length. A naturally occurring expression construct—for example the naturally occurring combination of a promoter with the corresponding gene—becomes a transgenic expression construct when it is modified by non-natural, synthetic “artificial” methods such as, for example, mutagenization. Such methods have been described (U.S. Pat. No. 5,565,350; WO 00/15815). For example a protein encoding nucleic acid molecule operably linked to a promoter, which is not the native promoter of this molecule, is considered to be heterologous with respect to the promoter. Preferably, heterologous DNA is not endogenous to or not naturally associated with the cell into which it is introduced, but has been obtained from another cell or has been synthesized. Heterologous DNA also includes an endogenous DNA sequence, which contains some modification, non-naturally occurring, multiple copies of an endogenous DNA sequence, or a DNA sequence which is not naturally associated with another DNA sequence physically linked thereto. Generally, although not necessarily, heterologous DNA encodes RNA or proteins that are not normally produced by the cell into which it is expressed.

Hybridization: The term “hybridization” as used herein includes “any process by which a strand of nucleic acid molecule joins with a complementary strand through base pairing.” (J. Coombs (1994) Dictionary of Biotechnology, Stockton Press, New York). Hybridization and the strength of hybridization (i.e., the strength of the association between the nucleic acid molecules) is impacted by such factors as the degree of complementarity between the nucleic acid molecules, stringency of the conditions involved, the  $T_m$  of the formed hybrid, and the G:C ratio within the nucleic acid molecules. As used herein, the term “ $T_m$ ” is used in reference to the “melting temperature.” The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. The equation for calculating the  $T_m$  of nucleic acid molecules is well known in the art. As indicated by standard references, a simple estimate of the  $T_m$  value may be calculated by the equation:  $T_m = 81.5 + 0.41(\% G+C)$ , when a nucleic acid molecule is in aqueous solution at 1 M NaCl [see e.g., Anderson and Young, Quantitative Filter Hybridization, in Nucleic Acid Hybridization (1985)]. Other references include more sophisticated computations, which take structural as well as sequence characteristics into account for the calculation of  $T_m$ . Stringent conditions, are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

Medium stringency conditions when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 68° C. in a solution consisting of 5×SSPE (43.8 g/L NaCl, 6.9 g/L NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O and 1.85 g/L EDTA, pH adjusted to 7.4 with NaOH), 1% SDS, 5×Denhardt’s reagent [50×Denhardt’s contains the following per 500 mL 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 µg/mL denatured salmon sperm DNA followed by washing (preferably for one times 15 minutes, more preferably two times 15 minutes, more preferably three times 15 minutes) in a solution comprising

1×SSC (1×SSC is 0.15 M NaCl plus 0.015 M sodium citrate) and 0.1% SDS at room temperature or—preferably 37° C.—when a DNA probe of preferably about 100 to about 500 nucleotides in length is employed.

High stringency conditions when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 68° C. in a solution consisting of 5×SSPE (43.8 g/L NaCl, 6.9 g/L NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O and 1.85 g/L EDTA, pH adjusted to 7.4 with NaOH), 1% SDS, 5×Denhardt’s reagent [50×Denhardt’s contains the following per 500 mL 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 µg/mL denatured salmon sperm DNA followed by washing (preferably for one times 15 minutes, more preferably two times 15 minutes, more preferably three times 15 minutes) in a solution comprising 0.1×SSC (1×SSC is 0.15 M NaCl plus 0.015 M sodium citrate) and 1% SDS at room temperature or—preferably 37° C.—when a DNA probe of preferably about 100 to about 500 nucleotides in length is employed.

Very high stringency conditions when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 68° C. in a solution consisting of 5×SSPE, 1% SDS, 5×Denhardt’s reagent and 100 µg/mL denatured salmon sperm DNA followed by washing (preferably for one times 15 minutes, more preferably two times 15 minutes, more preferably three times 15 minutes) in a solution comprising 0.1×SSC, and 1% SDS at 68° C., when a probe of preferably about 100 to about 500 nucleotides in length is employed.

“Identity”: “Identity” when used in respect to the comparison of two or more nucleic acid or amino acid molecules means that the sequences of said molecules share a certain degree of sequence similarity, the sequences being partially identical.

To determine the percentage identity (homology is herein used interchangeably) of two amino acid sequences or of two nucleic acid molecules, the sequences are written one underneath the other for an optimal comparison (for example gaps may be inserted into the sequence of a protein or of a nucleic acid in order to generate an optimal alignment with the other protein or the other nucleic acid).

The amino acid residues or nucleic acid molecules at the corresponding amino acid positions or nucleotide positions are then compared. If a position in one sequence is occupied by the same amino acid residue or the same nucleic acid molecule as the corresponding position in the other sequence, the molecules are homologous at this position (i.e. amino acid or nucleic acid “homology” as used in the present context corresponds to amino acid or nucleic acid “identity”). The percentage identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e. % homology = number of identical positions/total number of positions×100). The terms “homology” and “identity” are thus to be considered as synonyms.

For the determination of the percentage identity of two or more amino acids or of two or more nucleotide sequences several computer software programs have been developed. The identity of two or more sequences can be calculated with for example the software fasta, which presently has been used in the version fasta 3 (W. R. Pearson and D. J. Lipman, PNAS 85, 2444(1988); W. R. Pearson, Methods in Enzymology 183, 63 (1990); W. R. Pearson and D. J. Lipman, PNAS 85, 2444 (1988); W. R. Pearson, Enzymology 183, 63 (1990)). Another useful program for the calculation of identities of different sequences is the standard blast program, which is included in the Biomax pedant software

(Biomax, Munich, Federal Republic of Germany). This leads unfortunately sometimes to suboptimal results since blast does not always include complete sequences of the subject and the query. Nevertheless as this program is very efficient it can be used for the comparison of a huge number of sequences. The following settings are typically used for such a comparisons of sequences:

-p Program Name [String]; -d Database [String]; default=nr; -i Query File [File In]; default=stdin; -e Expectation value (E) [Real]; default=10.0; -m alignment view options: 0=pairwise; 1=query-anchored showing identities; 2=query-anchored no identities; 3=flat query-anchored, show identities; 4=flat query-anchored, no identities; 5=query-anchored no identities and blunt ends; 6=flat query-anchored, no identities and blunt ends; 7=XML Blast output; 8=tabular; 9 tabular with comment lines [Integer]; default=0; -o BLAST report Output File [File Out] Optional; default=stdout; -F Filter query sequence (DUST with blastn, SEG with others) [String]; default=T; -G Cost to open a gap (zero invokes default behavior) [Integer]; default=0; -E Cost to extend a gap (zero invokes default behavior) [Integer]; default=0; -X X dropoff value for gapped alignment (in bits) (zero invokes default behavior); blastn 30, megablast 20, tblastx 0, all others 15 [Integer]; default=0; -I Show GI's in defines [T/F]; default=F; -q Penalty for a nucleotide mismatch (blastn only) [Integer]; default=-3; -r Reward for a nucleotide match (blastn only) [Integer]; default=1; -v Number of database sequences to show one-line descriptions for (V) [Integer]; default=500; -b Number of database sequence to show alignments for (B) [Integer]; default=250; -f Threshold for extending hits, default if zero; blastp 11, blastn 0, blastx 12, tblastn 13; tblastx 13, megablast 0 [Integer]; default=0; -g Perform gapped alignment (not available with tblastx) [T/F]; default=T; -Q Query Genetic code to use [Integer]; default=1; -D DB Genetic code (for tblast[nx] only) [Integer]; default=1; -a Number of processors to use [Integer]; default=1; -O SeqAlign file [File Out] Optional; -J Believe the query define [T/F]; default=F; -M Matrix [String]; default=BLOSUM62; -W Word size, default if zero (blastn 11, megablast 28, all others 3) [Integer]; default=0; -z Effective length of the database (use zero for the real size) [Real]; default=0; -K Number of best hits from a region to keep (off by default, if used a value of 100 is recommended) [Integer]; default=0; -P 0 for multiple hit, 1 for single hit [Integer]; default=0; -Y Effective length of the search space (use zero for the real size) [Real]; default=0; -S Query strands to search against database (for blast[nx], and tblastx); 3 is both, 1 is top, 2 is bottom [Integer]; default=3; -T Produce HTML output [T/F]; default=F; -I Restrict search of database to list of GI's [String] Optional; -U Use lower case filtering of FASTA sequence [T/F] Optional; default=F; -y X dropoff value for ungapped extensions in bits (0.0 invokes default behavior); blastn 20, megablast 10, all others 7 [Real]; default=0.0; -Z X dropoff value for final gapped alignment in bits (0.0 invokes default behavior); blastn/megablast 50, tblastx 0, all others 25 [Integer]; default=0; -R PSI-TBLASTN checkpoint file [File In] Optional; -n MegaBlast search [T/F]; default=F; -L Location on query sequence [String] Optional; -A Multiple Hits window size, default if zero (blastn/megablast 0, all others 40 [Integer]; default=0; -w Frame shift penalty (OOF algorithm for blastx) [Integer]; default=0; -t Length of the largest intron allowed in tblastn for linking HSPs (0 disables linking) [Integer]; default=0.

Results of high quality are reached by using the algorithm of Needleman and Wunsch or Smith and Waterman. Therefore programs based on said algorithms are preferred.

Advantageously the comparisons of sequences can be done with the program PileUp (J. Mol. Evolution., 25, 351 (1987), Higgins et al., CABIOS 5, 151 (1989)) or preferably with the programs "Gap" and "Needle", which are both based on the algorithms of Needleman and Wunsch (J. Mol. Biol. 48; 443 (1970)), and "BestFit", which is based on the algorithm of Smith and Waterman (Adv. Appl. Math. 2; 482 (1981)). "Gap" and "BestFit" are part of the GCG software-package (Genetics Computer Group, 575 Science Drive, Madison, Wis., USA 53711 (1991); Altschul et al., (Nucleic Acids Res. 25, 3389 (1997)), "Needle" is part of the The European Molecular Biology Open Software Suite (EMBOSS) (Trends in Genetics 16 (6), 276 (2000)). Therefore preferably the calculations to determine the percentages of sequence identity are done with the programs "Gap" or "Needle" over the whole range of the sequences. The following standard adjustments for the comparison of nucleic acid sequences were used for "Needle": matrix: EDNAFULL, Gap\_penalty: 10.0, Extend\_penalty: 0.5. The following standard adjustments for the comparison of nucleic acid sequences were used for "Gap": gap weight: 50, length weight: 3, average match: 10.000, average mismatch: 0.000.

For example a sequence, which is said to have 80% identity with sequence SEQ ID NO: 1 at the nucleic acid level is understood as meaning a sequence which, upon comparison with the sequence represented by SEQ ID NO: 1 by the above program "Needle" with the above parameter set, has a 80% identity. The identity is calculated on the complete length of the query sequence, for example SEQ ID NO:1.

Isogenic: organisms (e.g., plants), which are genetically identical, except that they may differ by the presence or absence of a heterologous DNA sequence.

Isolated: The term "isolated" as used herein means that a material has been removed by the hand of man and exists apart from its original, native environment and is therefore not a product of nature. An isolated material or molecule (such as a DNA molecule or enzyme) may exist in a purified form or may exist in a non-native environment such as, for example, in a transgenic host cell. For example, a naturally occurring polynucleotide or polypeptide present in a living plant is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides can be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and would be isolated in that such a vector or composition is not part of its original environment. Preferably, the term "isolated" when used in relation to a nucleic acid molecule, as in "an isolated nucleic acid sequence" refers to a nucleic acid sequence that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in its natural source. Isolated nucleic acid molecule is nucleic acid molecule present in a form or setting that is different from that in which it is found in nature. In contrast, non-isolated nucleic acid molecules are nucleic acid molecules such as DNA and RNA, which are found in the state they exist in nature. For example, a given DNA sequence (e.g., a gene) is found on the host cell chromosome in proximity to neighboring genes; RNA sequences, such as a specific mRNA sequence encoding a specific protein, are found in the cell as a mixture with numerous other mRNAs, which encode a multitude of proteins. However, an isolated nucleic acid sequence comprising for example SEQ ID NO: 1 includes, by way of example, such nucleic acid sequences in cells which ordinarily contain SEQ ID NO:1 where the

nucleic acid sequence is in a chromosomal or extrachromosomal location different from that of natural cells, or is otherwise flanked by a different nucleic acid sequence than that found in nature. The isolated nucleic acid sequence may be present in single-stranded or double-stranded form. When an isolated nucleic acid sequence is to be utilized to express a protein, the nucleic acid sequence will contain at a minimum at least a portion of the sense or coding strand (i.e., the nucleic acid sequence may be single-stranded). Alternatively, it may contain both the sense and anti-sense strands (i.e., the nucleic acid sequence may be double-stranded).

Minimal Promoter: promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

Naturally occurring as used herein means a cell or molecule, for example a plant cell or nucleic acid molecule that occurs in a plant or organism which is not manipulated by man, hence which is for example neither mutated nor genetically engineered by man.

Non-coding: The term “non-coding” refers to sequences of nucleic acid molecules that do not encode part or all of an expressed protein. Non-coding sequences include but are not limited to introns, enhancers, promoter regions, 3' untranslated regions, and 5' untranslated regions.

Nucleic acids and nucleotides: The terms “Nucleic Acids” and “Nucleotides” refer to naturally occurring or synthetic or artificial nucleic acid or nucleotides. The terms “nucleic acids” and “nucleotides” comprise deoxyribonucleotides or ribonucleotides or any nucleotide analogue and polymers or hybrids thereof in either single- or double-stranded, sense or antisense form. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. The term “nucleic acid” is used interchangeably herein with “gene”, “cDNA”, “mRNA”, “oligonucleotide,” and “polynucleotide”. Nucleotide analogues include nucleotides having modifications in the chemical structure of the base, sugar and/or phosphate, including, but not limited to, 5-position pyrimidine modifications, 8-position purine modifications, modifications at cytosine exocyclic amines, substitution of 5-bromo-uracil, and the like; and 7-position sugar modifications, including but not limited to, sugar-modified ribonucleotides in which the 2'-OH is replaced by a group selected from H, OR, R, halo, SH, SR, NH<sub>2</sub>, NHR, NR<sub>2</sub>, or CN. Short hairpin RNAs (shRNAs) also can comprise non-natural elements such as non-natural bases, e.g., ionosin and xanthine, non-natural sugars, e.g., 7-methoxy ribose, or non-natural phosphodiester linkages, e.g., methylphosphonates, phosphorothioates and peptides.

Nucleic acid sequence: The phrase “nucleic acid sequence” refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5'- to the 3'-end. It includes chromosomal DNA, self-replicating plasmids, infectious polymers of DNA or RNA and DNA or RNA that performs a primarily structural role. “Nucleic acid sequence” also refers to a consecutive list of abbreviations, letters, characters or words, which represent nucleotides. In one embodiment, a nucleic acid can be a “probe” which is a relatively short nucleic acid, usually less than 100 nucleotides in length. Often a nucleic acid probe is from about 50 nucleotides in length to about 10 nucleotides in length. A “target region” of a nucleic acid is a portion of a nucleic acid that is identified to be of interest. A “coding

region” of a nucleic acid is the portion of the nucleic acid, which is transcribed and translated in a sequence-specific manner to produce into a particular polypeptide or protein when placed under the control of appropriate regulatory sequences. The coding region is said to encode such a polypeptide or protein.

Oligonucleotide: The term “oligonucleotide” refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof, as well as oligonucleotides having non-naturally-occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target and increased stability in the presence of nucleases. An oligonucleotide preferably includes two or more nucleomonomers covalently coupled to each other by linkages (e.g., phosphodiesters) or substitute linkages.

Overhang: An “overhang” is a relatively short single-stranded nucleotide sequence on the 5'- or 3'-hydroxyl end of a double-stranded oligonucleotide molecule (also referred to as an “extension,” “protruding end,” or “sticky end”).

Overlapping specificity: The term “overlapping specificity” when used herein related to expression specificity of two or more promoters means that the expression regulated by these promoters occur partly in the same plant tissues, developmental stages or conditions. For example, a promoter expressed in leaves and a promoter expressed in root and leaves have an overlap in expression specificity in the leaves of a plant.

Plant: is generally understood as meaning any eukaryotic single- or multi-celled organism or a cell, tissue, organ, part or propagation material (such as seeds or fruit) of same which is capable of photosynthesis. Included for the purpose of the invention are all genera and species of higher and lower plants of the Plant Kingdom. Annual, perennial, monocotyledonous and dicotyledonous plants are preferred. The term includes the mature plants, seed, shoots and seedlings and their derived parts, propagation material (such as seeds or microspores), plant organs, tissue, protoplasts, callus and other cultures, for example cell cultures, and any other type of plant cell grouping to give functional or structural units. Mature plants refer to plants at any desired developmental stage beyond that of the seedling. Seedling refers to a young immature plant at an early developmental stage. Annual, biennial, monocotyledonous and dicotyledonous plants are preferred host organisms for the generation of transgenic plants. The expression of genes is furthermore advantageous in all ornamental plants, useful or ornamental trees, flowers, cut flowers, shrubs or lawns. Plants which may be mentioned by way of example but not by limitation are angiosperms, bryophytes such as, for example, Hepaticae (liverworts) and Musci (mosses); Pteridophytes such as ferns, horsetail and club mosses; gymnosperms such as conifers, cycads, ginkgo and Gnetatae; algae such as Chlorophyceae, Phaeophyceae, Rhodophyceae, Myxophyceae, Xanthophyceae, Bacillariophyceae (diatoms), and Euglenophyceae. Preferred are plants which are used for food or feed purpose such as the families of the Leguminosae such as pea, alfalfa and soya; Gramineae such as rice, maize, wheat, barley, sorghum, millet, rye, triticale, or oats; the family of the Umbelliferae, especially the genus *Daucus*, very especially the species *carota* (carrot) and *Apium*, very especially the species *Graveolens dulce* (celery) and many others; the family of the Solanaceae, especially the genus *Lycopersicon*, very especially the species *esculentum* (tomato) and the genus *Solanum*, very especially

the species *tuberosum* (potato) and *melongena* (egg plant), and many others (such as tobacco); and the genus *Capsicum*, very especially the species *annuum* (peppers) and many others; the family of the Leguminosae, especially the genus *Glycine*, very especially the species *max* (soybean), alfalfa, pea, lucerne, beans or peanut and many others; and the family of the Cruciferae (Brassicaceae), especially the genus *Brassica*, very especially the species *napus* (oil seed rape), *campestris* (beet), *oleracea* cv Tastie (cabbage), *oleracea* cv Snowball Y (cauliflower) and *oleracea* cv Emperor (broccoli); and of the genus *Arabidopsis*, very especially the species *thaliana* and many others; the family of the Compositae, especially the genus *Lactuca*, very especially the species *sativa* (lettuce) and many others; the family of the Asteraceae such as sunflower, *Tagetes*, lettuce or *Calendula* and many other; the family of the Cucurbitaceae such as melon, pumpkin/squash or zucchini, and linseed. Further preferred are cotton, sugar cane, hemp, flax, chillies, and the various tree, nut and wine species.

Polypeptide: The terms “polypeptide”, “peptide”, “oligopeptide”, “polypeptide”, “gene product”, “expression product” and “protein” are used interchangeably herein to refer to a polymer or oligomer of consecutive amino acid residues.

Pre-protein: Protein, which is normally targeted to a cellular organelle, such as a chloroplast, and still comprising its transit peptide.

Primary transcript: The term “primary transcript” as used herein refers to a premature RNA transcript of a gene. A “primary transcript” for example still comprises introns and/or is not yet comprising a polyA tail or a cap structure and/or is missing other modifications necessary for its correct function as transcript such as for example trimming or editing.

Promoter: The terms “promoter”, or “promoter sequence” are equivalents and as used herein, refer to a DNA sequence which when ligated to a nucleotide sequence of interest is capable of controlling the transcription of the nucleotide sequence of interest into RNA. Such promoters can for example be found in the following public databases <http://www.grassius.org/grasspromdb.html>, <http://mendel.cs.rhul.ac.uk/mendel.php?topic=plantprom>, <http://ppdb.gene.nagoya-u.ac.jp/cgibin/index.cgi>. Promoters listed there may be addressed with the methods of the invention and are hereby included by reference. A promoter is located 5' (i.e., upstream), proximal to the transcriptional start site of a nucleotide sequence of interest whose transcription into mRNA it controls, and provides a site for specific binding by RNA polymerase and other transcription factors for initiation of transcription. Said promoter comprises for example the at least 10 kb, for example 5 kb or 2 kb proximal to the transcription start site. It may also comprise the at least 1500 bp proximal to the transcriptional start site, preferably the at least 1000 bp, more preferably the at least 500 bp, even more preferably the at least 400 bp, the at least 300 bp, the at least 200 bp or the at least 100 bp. In a further preferred embodiment, the promoter comprises the at least 50 bp proximal to the transcription start site, for example, at least 25 bp. The promoter does not comprise exon and/or intron regions or 5' untranslated regions. The promoter may for example be heterologous or homologous to the respective plant. A polynucleotide sequence is “heterologous to” an organism or a second polynucleotide sequence if it originates from a foreign species, or, if from the same species, is modified from its original form. For example, a promoter operably linked to a heterologous coding sequence refers to a coding sequence from a species different from that from

which the promoter was derived, or, if from the same species, a coding sequence which is not naturally associated with the promoter (e.g. a genetically engineered coding sequence or an allele from a different ecotype or variety). Suitable promoters can be derived from genes of the host cells where expression should occur or from pathogens for this host cells (e.g., plants or plant pathogens like plant viruses). A plant specific promoter is a promoter suitable for regulating expression in a plant. It may be derived from a plant but also from plant pathogens or it might be a synthetic promoter designed by man. If a promoter is an inducible promoter, then the rate of transcription increases in response to an inducing agent. Also, the promoter may be regulated in a tissue-specific or tissue preferred manner such that it is only or predominantly active in transcribing the associated coding region in a specific tissue type(s) such as leaves, roots or meristem. The term “tissue specific” as it applies to a promoter refers to a promoter that is capable of directing selective expression of a nucleotide sequence of interest to a specific type of tissue (e.g., petals) in the relative absence of expression of the same nucleotide sequence of interest in a different type of tissue (e.g., roots). Tissue specificity of a promoter may be evaluated by, for example, operably linking a reporter gene to the promoter sequence to generate a reporter construct, introducing the reporter construct into the genome of a plant such that the reporter construct is integrated into every tissue of the resulting transgenic plant, and detecting the expression of the reporter gene (e.g., detecting mRNA, protein, or the activity of a protein encoded by the reporter gene) in different tissues of the transgenic plant. The detection of a greater level of expression of the reporter gene in one or more tissues relative to the level of expression of the reporter gene in other tissues shows that the promoter is specific for the tissues in which greater levels of expression are detected. The term “cell type specific” as applied to a promoter refers to a promoter, which is capable of directing selective expression of a nucleotide sequence of interest in a specific type of cell in the relative absence of expression of the same nucleotide sequence of interest in a different type of cell within the same tissue. The term “cell type specific” when applied to a promoter also means a promoter capable of promoting selective expression of a nucleotide sequence of interest in a region within a single tissue. Cell type specificity of a promoter may be assessed using methods well known in the art, e.g., GUS activity staining, GFP protein or immunohistochemical staining. The term “constitutive” when made in reference to a promoter or the expression derived from a promoter means that the promoter is capable of directing transcription of an operably linked nucleic acid molecule in the absence of a stimulus (e.g., heat shock, chemicals, light, etc.) in the majority of plant tissues and cells throughout substantially the entire lifespan of a plant or part of a plant. Typically, constitutive promoters are capable of directing expression of a transgene in substantially any cell and any tissue.

Promoter specificity: The term “specificity” when referring to a promoter means the pattern of expression conferred by the respective promoter. The specificity describes the tissues and/or developmental status of a plant or part thereof, in which the promoter is conferring expression of the nucleic acid molecule under the control of the respective promoter. Specificity of a promoter may also comprise the environmental conditions, under which the promoter may be activated or down-regulated such as induction or repression by biological or environmental stresses such as cold, drought, wounding or infection.

Purified: As used herein, the term “purified” refers to molecules, either nucleic or amino acid sequences that are removed from their natural environment, isolated or separated. “Substantially purified” molecules are at least 60% free, preferably at least 75% free, and more preferably at least 90% free from other components with which they are naturally associated. A purified nucleic acid sequence may be an isolated nucleic acid sequence.

Recombinant: The term “recombinant” with respect to nucleic acid molecules refers to nucleic acid molecules produced by recombinant DNA techniques. Recombinant nucleic acid molecules as such do not exist in nature but are modified, changed, mutated or otherwise manipulated by man. A “recombinant nucleic acid molecule” is a non-naturally occurring nucleic acid molecule that differs in sequence from a naturally occurring nucleic acid molecule by at least one nucleic acid. The term “recombinant nucleic acid molecule” may also comprise a “recombinant construct” which comprises, preferably operably linked, a sequence of nucleic acid molecules, which are not naturally occurring in that order wherein each of the nucleic acid molecules may or may not be a recombinant nucleic acid molecule. Preferred methods for producing said recombinant nucleic acid molecule may comprise cloning techniques, directed or non-directed mutagenesis, synthesis or recombination techniques.

Sense: The term “sense” is understood to mean a nucleic acid molecule having a sequence which is complementary or identical to a target sequence, for example a sequence which binds to a protein transcription factor and which is involved in the expression of a given gene. According to a preferred embodiment, the nucleic acid molecule comprises a gene of interest and elements allowing the expression of the said gene of interest.

Starting sequence: The term “starting sequence” when used herein defines the sequence of a promoter of a defined specificity which is used as a reference sequence for analysis of the presence of motives. The starting sequence is referred to for the definition of the degree of identity to the sequences of the promoters of the invention. The starting sequence could be any wild-type, naturally occurring promoter sequence or any artificial promoter sequence. The sequence of a synthetic promoter sequence produced with the method of the invention may also be used as a starting sequence.

Substantially complementary: In its broadest sense, the term “substantially complementary”, when used herein with respect to a nucleotide sequence in relation to a reference or target nucleotide sequence, means a nucleotide sequence having a percentage of identity between the substantially complementary nucleotide sequence and the exact complementary sequence of said reference or target nucleotide sequence of at least 60%, more desirably at least 70%, more desirably at least 80% or 85%, preferably at least 90%, more preferably at least 93%, still more preferably at least 95% or 96%, yet still more preferably at least 97% or 98%, yet still more preferably at least 99% or most preferably 100% (the later being equivalent to the term “identical” in this context). Preferably identity is assessed over a length of at least 19 nucleotides, preferably at least 50 nucleotides, more preferably the entire length of the nucleic acid sequence to said reference sequence (if not specified otherwise below). Sequence comparisons are carried out using default GAP analysis with the University of Wisconsin GCG, SEQWEB application of GAP, based on the algorithm of Needleman and Wunsch (Needleman and Wunsch (1970) J Mol. Biol. 48: 443-453; as defined above). A nucleotide sequence “substantially complementary” to a reference nucleotide

sequence hybridizes to the reference nucleotide sequence under low stringency conditions, preferably medium stringency conditions, most preferably high stringency conditions (as defined above).

Transgene: The term “transgene” as used herein refers to any nucleic acid sequence, which is introduced into the genome of a cell by experimental manipulations. A transgene may be an “endogenous DNA sequence,” or a “heterologous DNA sequence” (i.e., “foreign DNA”). The term “endogenous DNA sequence” refers to a nucleotide sequence, which is naturally found in the cell into which it is introduced so long as it does not contain some modification (e.g., a point mutation, the presence of a selectable marker gene, etc.) relative to the naturally-occurring sequence.

Transgenic: The term transgenic when referring to an organism means transformed, preferably stably transformed, with a recombinant DNA molecule that preferably comprises a suitable promoter operatively linked to a DNA sequence of interest.

Vector: As used herein, the term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid molecule to which it has been linked. One type of vector is a genomic integrated vector, or “integrated vector”, which can become integrated into the chromosomal DNA of the host cell. Another type of vector is an episomal vector, i.e., a nucleic acid molecule capable of extra-chromosomal replication. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as “expression vectors”. In the present specification, “plasmid” and “vector” are used interchangeably unless otherwise clear from the context. Expression vectors designed to produce RNAs as described herein in vitro or in vivo may contain sequences recognized by any RNA polymerase, including mitochondrial RNA polymerase, RNA pol I, RNA pol II, and RNA pol III. These vectors can be used to transcribe the desired RNA molecule in the cell according to this invention. A plant transformation vector is to be understood as a vector suitable in the process of plant transformation.

Wild-type: The term “wild-type”, “natural” or “natural origin” means with respect to an organism, polypeptide, or nucleic acid sequence, that said organism is naturally occurring or available in at least one naturally occurring organism which is not changed, mutated, or otherwise manipulated by man.

## EXAMPLES

### Chemicals and Common Methods

Unless indicated otherwise, cloning procedures carried out for the purposes of the present invention including restriction digest, agarose gel electrophoresis, purification of nucleic acids, ligation of nucleic acids, transformation, selection and cultivation of bacterial cells were performed as described (Sambrook et al., 1989). Sequence analyses of recombinant DNA were performed with a laser fluorescence DNA sequencer (Applied Biosystems, Foster City, Calif., USA) using the Sanger technology (Sanger et al., 1977). Unless described otherwise, chemicals and reagents were obtained from Sigma Aldrich (Sigma Aldrich, St. Louis, USA), from Promega (Madison, Wis., USA), Duchefa (Haarlem, The Netherlands) or Invitrogen (Carlsbad, Calif., USA). Restriction endonucleases were from New England Biolabs (Ipswich, Mass., USA) or Roche Diagnostics GmbH



(Penzberg, Germany). Oligonucleotides were synthesized by Eurofins MWG Operon (Ebersberg, Germany).

### Example 1

#### 1.1 Directed Permutation of the Promoter Sequence

Using publicly available data, two promoters showing seed specific expression in plants were selected for analyzing the effects of sequence permutation in periodic intervals throughout the full length of the promoter DNA sequence (WO2009016202, WO2009133145). The wildtype or starting sequences of the *Phaseolus vulgaris* p-PvARC5 (SEQ ID NO 1) (with the prefix p- denoting promoter) and the *Vicia faba* p-VfSBP (SEQ ID NO 3) promoters were analyzed and annotated for the occurrence of motives, boxes, cis-regulatory elements using e.g. the GEMS Launcher Software (www.genomatix.de) with default parameters (Core similarity 0.75, matrix similarity 0.75)

The “core sequence” of a matrix is defined as the usually 4 consecutive highest conserved positions of the matrix.

The core similarity is calculated as described here and in the papers related to MatInspector (Cartharius K, et al. (2005) Bioinformatics 21; Cartharius K (2005), DNA Press; Quandt K, et al (1995) Nucleic Acids Res. 23.

The maximum core similarity of 1.0 is only reached when the highest conserved bases of a matrix match exactly in the sequence. More important than the core similarity is the matrix similarity which takes into account all bases over the whole matrix length. The matrix similarity is calculated as described here and in the MatInspector paper. A perfect match to the matrix gets a score of 1.00 (each sequence position corresponds to the highest conserved nucleotide at that position in the matrix), a “good” match to the matrix has a similarity of >0.80.

Mismatches in highly conserved positions of the matrix decrease the matrix similarity more than mismatches in less conserved regions.

Opt gives the Optimized matrix threshold: This matrix similarity is the optimized value defined in a way that a minimum number of matches is found in non-regulatory test sequences (i.e. with this matrix similarity the number of false positive matches is minimized). This matrix similarity is used when the user checks “Optimized” as the matrix similarity threshold for MatInspector.

In the following, the DNA sequences of the promoters were permuted according to the method of the invention to yield p-PvArc5\_perm (SEQ ID NO 2) and p-VfSBP\_perm (SEQ ID NO 4). In case of the p-PvArc5 promoter 6.6% of the motives not associated with seed specific/preferential expression and transcription initiation have been altered, in case of the p-VfSBP 7.8%. DNA permutation was conducted in a way to not affect cis regulatory elements which have been associated previously with seed specific gene expression or initiation of transcription and permutations were distributed periodically over the full promoter DNA sequence with less than 46 nucleotides between permuted nucleotide positions and within a stretch of 5 nucleotides having at least one nucleotide permuted. Permutations were carried out with the aim to keep most of the cis regulatory elements, boxes, motives present in the native promoter and to avoid creating new putative cis regulatory elements, boxes, motives.

The list of motives, boxes, cis regulatory elements in the PvARC5 promoters before and after the permutation are shown in Table 1 and 2.

The list of motives, boxes, cis regulatory elements in the VfSBP promoters before and after the permutation are shown in Table 3 and 4.

Empty lines resemble motives, boxes, cis regulatory elements not found in one sequence but present in the corresponding sequence, hence, motives, boxes, cis regulatory elements that were deleted from the starting sequence or that were introduced into the permuted sequence.

TABLE 1

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promoter			Position				
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
PSPSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	9-25	(+)	1	0.862
PSIDDF	ID domain factors	P\$ID1.01	0.92	36-48	(-)	1	0.922
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	47-63	(+)	1	0.887
P\$RAV5	5'-part of bipartite RAV1 binding site	P\$RAV1-5.01	0.96	48-58	(+)	1	0.96
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	52-68	(-)	1	0.932
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	75-85	(+)	0.97	0.988
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	84-94	(-)	1	0.963
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXL.01	0.80	87-101	(+)	0.84	0.806
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	106-116	(+)	1	0.99
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	108-122	(+)	0.81	0.884
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	110-120	(-)	1	0.963
P\$TEFB	TEF-box	P\$TEF1.01	0.76	111-131	(-)	0.96	0.761
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	113-127	(+)	0.77	0.856
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	121-137	(-)	1	0.964
P\$GAGA	GAGA elements	P\$GAGABP.01	0.75	125-149	(-)	0.75	0.768

TABLE 1-continued

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promotor			Position				
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	126-140	(+)	1	0.799
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	144-154	(-)	1	0.923
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	147-157	(-)	1	0.928
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$LTATA.01	0.82	151-167	(+)	1	0.839
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	164-174	(-)	1	0.898
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	175-191	(+)	0.75	0.872
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	177-187	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	177-187	(-)	1	1
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$ATATA.01	0.78	184-200	(+)	0.75	0.797
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	186-200	(-)	0.75	0.857
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	213-227	(-)	1	0.826
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	233-251	(+)	0.75	0.824
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	238-254	(+)	0.82	0.798
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	261-271	(-)	1	0.851
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	264-280	(+)	1	0.774
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$ATATA.01	0.78	267-283	(+)	1	0.872
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	298-310	(-)	1	0.872
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	303-319	(-)	1	0.953
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	319-335	(+)	0.89	0.762
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$TGA1.01	0.90	327-347	(-)	1	0.909
P\$GTBX	GT-box elements	P\$GT1.01	0.85	337-353	(+)	1	0.854
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	337-353	(-)	1	0.935
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	351-367	(-)	1	0.919
P\$GTBX	GT-box elements	P\$S1F.01	0.79	362-378	(-)	0.75	0.797
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	367-377	(-)	1	0.788
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	367-377	(+)	1	0.926
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	367-383	(+)	1	0.894
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	369-385	(+)	1	0.827
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	371-381	(-)	1	1
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	396-412	(-)	1	0.857
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	397-407	(+)	1	0.921

TABLE 1-continued

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promoter				Position			
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	401-411	(-)	1	0.916
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	403-419	(-)	1	0.9
P\$MYBS	MYB proteins with single DNA binding repeat	P\$OSMYBS.01	0.82	416-432	(+)	0.75	0.837
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	440-454	(-)	0.75	0.854
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	461-479	(-)	0.75	0.826
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	468-478	(+)	1	0.892
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	473-489	(-)	1	0.913
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	476-490	(-)	1	0.889
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	482-498	(+)	1	0.831
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	499-513	(-)	1	0.91
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	499-517	(-)	1	0.878
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	509-525	(-)	1	0.885
P\$GARP	Myb-related DNA binding proteins (Golden2, ARR, Psr)	P\$ARR10.01	0.97	540-548	(+)	1	0.976
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	558-568	(-)	1	0.775
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	558-574	(-)	1	0.865
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	558-568	(-)	0.88	0.927
P\$EINL	Ethylen insensitive 3 like factors	P\$TEIL.01	0.92	572-580	(+)	1	0.921
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	583-593	(+)	0.94	0.977
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	583-593	(-)	0.83	0.94
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	607-623	(+)	1	0.772
P\$IBOX	Plant I-Box sites	P\$IBOX.01	0.81	610-626	(+)	0.75	0.824
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.90	613-629	(-)	1	0.953
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	616-632	(+)	1	0.942
P\$TEFB	TEF-box	P\$TEF1.01	0.76	616-636	(+)	0.96	0.778
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	625-641	(-)	1	0.859
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	631-645	(+)	1	0.927
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	632-646	(-)	1	0.929
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	646-662	(-)	0.75	0.825
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	648-664	(+)	1	0.791
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	649-663	(-)	1	0.902

TABLE 1-continued

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promotor			Position				
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	654-670	(+)	1	0.979
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	682-692	(-)	1	0.975
P\$TEFB	TEF-box	P\$TEF1.01	0.76	696-716	(-)	0.84	0.78
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	699-715	(-)	1	0.88
P\$LEGB	Legumin Box family	P\$RY.01	0.87	704-730	(+)	1	0.94
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	716-736	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	717-737	(+)	1	1
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	719-735	(-)	0.75	0.857
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.02	0.84	722-742	(-)	0.75	0.862
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	739-757	(-)	0.86	0.943
P\$OPAQ	Opaque-2 like transcriptional activators	P\$GCN4.01	0.81	745-761	(-)	1	0.85
P\$AREF	Auxin response element	P\$ARE.01	0.93	747-759	(+)	1	0.941
P\$TEFB	TEF-box	P\$TEF1.01	0.76	783-803	(-)	0.84	0.78
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	786-802	(-)	1	0.876
P\$LEGB	Legumin Box family	P\$RY.01	0.87	788-814	(-)	1	0.929
P\$LEGB	Legumin Box family	P\$RY.01	0.87	791-817	(+)	1	0.984
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	796-820	(+)	1	0.812
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$CPRF.01	0.95	803-823	(-)	1	0.989
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$CPRF.01	0.95	804-824	(+)	1	0.98
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	804-822	(-)	1	0.956
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	805-821	(+)	1	0.874
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$PIF3.01	0.82	805-823	(+)	1	0.914
P\$OPAQ	Opaque-2 like transcriptional activators	P\$RITA1.01	0.95	805-821	(-)	1	0.992
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	806-822	(-)	1	0.977
P\$OPAQ	Opaque-2 like transcriptional activators	P\$RITA1.01	0.95	806-822	(+)	1	0.973
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSTF.01	0.73	809-829	(-)	0.85	0.747
P\$GTBX	GT-box elements	P\$S1F.01	0.79	823-839	(-)	1	0.794
P\$LFYB	LFY binding site	P\$LFY.01	0.93	839-851	(-)	0.91	0.935

TABLE 1-continued

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promoter			Position				
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$LEGB	Legumin Box family	P\$RY.01	0.87	840-866	(-)	1	0.948
P\$LEGB	Legumin Box family	P\$RY.01	0.87	843-869	(+)	1	0.966
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	847-873	(+)	1	0.779
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	855-875	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	856-876	(+)	1	1
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	858-874	(-)	0.75	0.857
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.02	0.84	861-881	(-)	0.75	0.862
P\$SALT	Salt/drought responsive elements	P\$ALFIN1.02	0.95	871-885	(-)	1	0.963
P\$LEGB	Legumin Box family	P\$RY.01	0.87	895-921	(+)	1	0.927
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	907-927	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	908-928	(+)	1	0.938
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	910-926	(-)	0.75	0.857
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.02	0.84	913-933	(-)	0.75	0.871
P\$MADS	MADS box proteins	P\$SQUA.01	0.90	960-980	(-)	1	0.908
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	963-979	(+)	1	0.856
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	972-982	(+)	1	0.858
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	974-988	(-)	0.83	0.886
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	974-990	(+)	0.75	0.83
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	976-992	(+)	1	0.843
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	983-999	(-)	1	0.787
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	984-1002	(-)	1	0.818
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	991-1001	(+)	1	0.989
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	991-1001	(-)	1	0.943
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	992-1006	(+)	1	0.913
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	1003-1015	(+)	1	0.881
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSTF.01	0.73	1004-1024	(+)	1	0.776
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$UPRE.01	0.86	1009-1029	(-)	1	0.974

TABLE 1-continued

Boxes and Motifs identified in the starting sequence of the PvARC5 promoter							
PvARC5 promoter			Position				
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$TGA1.01	0.90	1010-1030	(+)	1	0.991
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	1011-1027	(+)	1	0.828
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	1011-1027	(-)	1	0.99
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	1012-1028	(+)	0.95	0.893
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	1013-1037	(-)	1	0.771
P\$LEGB	Legumin Box family	P\$LEGB.01	0.65	1025-1051	(+)	1	0.656
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1042-1052	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1042-1052	(-)	1	1
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1045-1061	(+)	1	0.904
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1070-1080	(-)	0.97	0.949
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	1093-1107	(-)	1	0.952
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1098-1114	(-)	0.75	0.843
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	1102-1120	(-)	1	0.791
P\$MADS	MADS box proteins	P\$SQUA.01	0.90	1108-1128	(-)	1	0.928
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1111-1125	(+)	1	0.961
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1112-1128	(+)	1	0.968
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1130-1156	(-)	1	0.922
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	1135-1145	(+)	1	1
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1138-1164	(-)	1	0.914
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	1138-1162	(+)	0.75	0.794
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1141-1157	(+)	0.75	0.833

TABLE 2

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promoter permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	9-25	(+)	1	0.862
P\$IDDF	ID domain factors	P\$ID1.01	0.92	36-48	(-)	1	0.922
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	47-63	(+)	1	0.887
P\$RAV5	5'-part of bipartite RAV1 binding site	P\$RAV1-5.01	0.96	48-58	(+)	1	0.96
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	52-68	(-)	1	0.932
P\$STKM	Storekeeper motif	P\$STK.01	0.85	58-72	(+)	0.79	0.894

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$MYBL	MYB-like proteins	P\$MYBPH3.01	0.80	59-75	(+)	0.75	0.806
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	62-78	(+)	0.89	0.791
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	75-85	(+)	0.97	0.988
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	84-94	(-)	1	0.963
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXL.01	0.80	87-101	(+)	0.84	0.806
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	106-116	(+)	1	0.99
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	108-122	(+)	0.81	0.884
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	110-120	(-)	1	0.963
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	121-137	(-)	1	0.939
P\$GAGA	GAGA elements	P\$GAGABP.01	0.75	125-149	(-)	0.75	0.764
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	126-140	(+)	1	0.799
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	144-154	(-)	1	0.923
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	147-157	(-)	1	0.928
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	149-165	(+)	1	0.78
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	151-167	(+)	1	0.825
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	164-174	(-)	1	0.898
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	175-191	(+)	0.75	0.872
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	177-187	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	177-187	(-)	1	1
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	184-200	(+)	0.75	0.797
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	186-200	(-)	0.75	0.857
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	188-204	(-)	1	0.843
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	213-227	(-)	1	0.826
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	221-237	(+)	1	1
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	233-251	(+)	0.75	0.824
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	238-254	(+)	0.82	0.798
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	243-261	(-)	0.75	0.824
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	250-260	(+)	1	0.892
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	257-273	(+)	1	0.881
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	261-271	(-)	1	0.851
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	264-280	(+)	1	0.774
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	267-283	(+)	1	0.872
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	289-305	(-)	1	0.919
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	298-310	(-)	1	0.872

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	303-319	(-)	1	0.953
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$TGA1.01	0.90	327-347	(-)	1	0.909
P\$GTBX	GT-box elements	P\$GT1.01	0.85	337-353	(+)	1	0.854
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	337-353	(-)	1	0.935
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	342-358	(-)	1	0.896
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	343-353	(-)	1	0.869
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	343-353	(-)	0.88	0.915
P\$GTBX	GT-box elements	P\$S1F.01	0.79	344-360	(-)	0.75	0.827
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	345-355	(+)	0.97	0.945
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	351-367	(-)	1	0.919
P\$GTBX	GT-box elements	P\$S1F.01	0.79	362-378	(-)	0.75	0.797
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	367-377	(-)	1	0.788
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	367-377	(+)	1	0.926
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	367-383	(+)	1	0.894
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	369-385	(+)	1	0.827
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	371-381	(-)	1	1
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	376-392	(-)	0.86	0.924
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	387-401	(+)	1	0.851
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	392-410	(+)	1	0.864
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	396-412	(-)	1	0.852
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	397-407	(+)	1	0.911
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	401-411	(-)	1	0.916
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	403-419	(-)	1	0.9
P\$MYBS	MYB proteins with single DNA binding repeat	P\$OSMYBS.01	0.82	416-432	(+)	0.75	0.829
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	420-436	(-)	0.75	0.821
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$ATATA.01	0.78	426-442	(+)	0.75	0.819
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	426-442	(-)	1	0.902
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	428-444	(-)	1	0.772
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	428-448	(+)	0.77	0.692
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	440-454	(-)	0.75	0.854



TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	455-465	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	455-465	(-)	1	0.979
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	461-479	(-)	0.75	0.815
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	468-478	(+)	1	0.901
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$VTATA.01	0.90	473-489	(-)	1	0.913
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	476-490	(-)	1	0.889
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$ATATA.01	0.78	489-505	(-)	0.75	0.825
PSL1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	491-507	(+)	1	0.791
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	492-506	(-)	1	0.902
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	498-512	(+)	0.76	0.862
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	499-513	(-)	1	0.909
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	499-517	(-)	1	0.827
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	509-525	(-)	1	0.885
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	520-532	(-)	1	0.905
P\$WBXF	W Box family	P\$WRKY.01	0.92	526-542	(-)	1	0.936
P\$GARP	Myb-related DNA binding proteins (Golden2, ARR, Psr)	P\$ARR10.01	0.97	540-548	(+)	1	0.976
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	558-568	(-)	1	0.775
PSL1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	558-574	(-)	1	0.865
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	558-568	(-)	0.88	0.927
P\$EINL	Ethylen insensitive 3 like factors	P\$TEIL.01	0.92	572-580	(+)	1	0.921
P\$SBPD	SBP-domain proteins	P\$SBP.01	0.88	573-589	(+)	1	0.885
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	583-593	(+)	0.94	0.977
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	583-593	(-)	0.83	0.94
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	591-609	(-)	0.86	0.958
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	593-609	(+)	1	0.838
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$VTATA.02	0.89	603-619	(+)	1	0.89
PSL1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	607-623	(+)	1	0.772
PSIBOX	Plant I-Box sites	PSIBOX.01	0.81	610-626	(+)	0.75	0.824
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.90	613-629	(-)	1	0.953
PSIBOX	Plant I-Box sites	P\$GATA.01	0.93	616-632	(+)	1	0.942

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$TEFB	TEF-box	P\$TEF1.01	0.76	616-636	(+)	0.96	0.778
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	625-641	(-)	1	0.861
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	631-645	(+)	1	0.927
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	632-646	(-)	1	0.929
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	648-664	(+)	1	0.822
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	649-663	(-)	1	0.923
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	654-670	(+)	1	0.979
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	682-692	(-)	1	0.975
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	689-705	(+)	1	0.884
P\$TEFB	TEF-box	P\$TEF1.01	0.76	696-716	(-)	0.84	0.779
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	699-715	(-)	1	0.88
P\$LEGB	Legumin Box family	P\$RY.01	0.87	704-730	(+)	1	0.94
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	716-736	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	717-737	(+)	1	1
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	719-735	(-)	0.75	0.857
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.02	0.84	722-742	(-)	0.75	0.862
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$HBP1B.01	0.83	734-754	(+)	0.77	0.852
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	739-757	(-)	0.86	0.953
P\$ABRE	ABA response elements	P\$ABF1.01	0.79	741-757	(-)	0.75	0.796
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	741-757	(+)	1	0.871
P\$OPAQ	Opaque-2 like transcriptional activators	P\$GCN4.01	0.81	745-761	(-)	1	0.85
P\$AREF	Auxin response element	P\$ARE.01	0.93	747-759	(+)	1	0.941
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	754-770	(+)	1	0.933
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	757-767	(+)	1	0.943
P\$WBXF	W Box family	P\$WRKY.01	0.92	780-796	(+)	1	0.942
P\$TEFB	TEF-box	P\$TEF1.01	0.76	783-803	(-)	0.84	0.779
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	786-802	(-)	1	0.876
P\$LEGB	Legumin Box family	P\$RY.01	0.87	788-814	(-)	1	0.929
P\$LEGB	Legumin Box family	P\$RY.01	0.87	791-817	(+)	1	0.984
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	796-820	(+)	1	0.812
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$CPRF.01	0.95	803-823	(-)	1	0.989
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$CPRF.01	0.95	804-824	(+)	1	0.98

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	804-822	(-)	1	0.956
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	805-821	(+)	1	0.874
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$PIF3.01	0.82	805-823	(+)	1	0.922
P\$OPAQ	Opaque-2 like transcriptional activators	P\$RITA1.01	0.95	805-821	(-)	1	0.992
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	806-822	(-)	1	0.977
P\$OPAQ	Opaque-2 like transcriptional activators	P\$RITA1.01	0.95	806-822	(+)	1	0.973
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	809-829	(-)	1	0.819
P\$GTBX	GT-box elements	P\$S1F.01	0.79	823-839	(-)	1	0.802
P\$LFYB	LFY binding site	P\$LFY.01	0.93	839-851	(-)	0.91	0.936
P\$LEGB	Legumin Box family	P\$RY.01	0.87	840-866	(-)	1	0.948
P\$LEGB	Legumin Box family	P\$RY.01	0.87	843-869	(+)	1	0.966
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	847-873	(+)	1	0.779
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	855-875	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	856-876	(+)	1	1
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	858-874	(-)	0.75	0.857
P\$GCCF	GCC box family	P\$ERE_JERE.01	0.85	870-882	(-)	0.81	0.86
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	880-894	(-)	1	0.827
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	881-897	(+)	0.81	0.867
P\$LEGB	Legumin Box family	P\$RY.01	0.87	895-921	(+)	1	0.924
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.01	0.77	907-927	(-)	0.75	0.856
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$ROM.01	0.85	908-928	(+)	1	0.938
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	910-926	(-)	0.75	0.864
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$BZIP910.02	0.84	913-933	(-)	0.75	0.871
P\$SBPD	SBP-domain proteins	P\$SBP.01	0.88	939-955	(+)	1	0.887
P\$EINL	Ethylene insensitive 3 like factors	P\$TEIL.01	0.92	942-950	(+)	0.84	0.922
P\$MADS	MADS box proteins	P\$SQUA.01	0.90	960-980	(-)	1	0.908
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	963-979	(+)	1	0.856
P\$LREM	Light responsive element motif, not modulated	P\$RAP22.01	0.85	972-982	(+)	1	0.858

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
O\$PTBP	by different light qualities Plant TATA binding protein factor	O\$PTATA.01	0.88	974-988	(-)	0.83	0.905
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$ATATA.01	0.78	974-990	(+)	0.75	0.83
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$MTATA.01	0.84	976-992	(+)	1	0.855
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	983-999	(-)	1	0.867
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	984-1002	(-)	1	0.81
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	991-1001	(+)	1	0.989
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$SHAHB4.01	0.87	991-1001	(-)	1	0.943
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	992-1006	(+)	1	0.913
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1004-1024	(+)	1	0.827
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$UPRE.01	0.86	1009-1029	(-)	1	0.974
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$TGA1.01	0.90	1010-1030	(+)	1	0.991
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	1011-1027	(+)	1	0.828
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	1011-1027	(-)	1	0.99
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	1012-1028	(+)	0.95	0.893
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	1013-1037	(-)	1	0.771
P\$LEGB	Legumin Box family	P\$LEGB.01	0.65	1025-1051	(+)	1	0.656
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1042-1052	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1042-1052	(-)	1	1
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1045-1061	(+)	1	0.888
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1046-1062	(-)	1	0.888
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1060-1076	(+)	1	0.949
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1070-1080	(-)	0.97	0.949
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$TANAC69.01	0.68	1078-1100	(+)	1	0.775
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	1093-1107	(-)	1	0.949
P\$MADS	MADS box proteins	P\$SQUA.01	0.90	1097-1117	(+)	1	0.908
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	1102-1120	(-)	1	0.791
P\$MADS	MADS box proteins	P\$SQUA.01	0.90	1108-1128	(-)	1	0.928

TABLE 2-continued

Boxes and Motifs identified in the permuted sequence of the PvARC5 promoter.							
PvARC5 promotor permuted							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1111-1125	(+)	1	0.961
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$VTATA.01	0.90	1112-1128	(+)	1	0.968
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1130-1156	(-)	1	0.932
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1138-1164	(-)	1	0.914
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	1138-1162	(+)	0.75	0.794
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1141-1157	(+)	0.75	0.833

Preferably associated boxes are annotated in line 38, 43, 116, 121, 124, 128, 129, 137, 138, 143, 145, 146, 147, 151, 152, 153, 156, 162, 165, 175, 184, 186, 188, 203 and 205 of tables 1 and 2. Essential boxes are annotated in line 83, 111, 112, 172 and 201 of tables 1 and 2.

TABLE 3

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.90	12-28	(+)	1	0.918
P\$GAGA	GAGA elements	P\$BPC.01	1.00	25-49	(-)	1	1
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	80-106	(-)	1	0.805
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	85-101	(-)	1	0.843
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	101-117	(-)	1	0.883
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	118-130	(+)	1	0.897
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$HBP1B.01	0.83	138-158	(+)	1	0.834
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	165-181	(-)	0.78	0.788
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$TANAC69.01	0.68	173-195	(-)	0.81	0.729
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	174-194	(-)	0.98	0.862
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	175-195	(+)	0.98	0.863
P\$TCPF	DNA-binding proteins with the plant specific TCP-domain	P\$ATTCP20.01	0.94	189-201	(+)	1	0.968

TABLE 3-continued

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	194-210	(-)	0.89	0.8
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	198-208	(+)	0.83	0.936
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	207-223	(+)	0.75	0.811
P\$EINL	Ethylen insensitive 3 like factors	P\$TEIL.01	0.92	215-223	(-)	0.96	0.924
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$HBP1A.01	0.88	217-237	(-)	1	0.908
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	218-238	(+)	1	0.963
P\$GTBX	GT-box elements	P\$S1F.01	0.79	218-234	(+)	1	0.821
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	219-235	(+)	1	0.825
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	221-245	(-)	1	0.803
P\$CE1F	Coupling element 1 binding factors	P\$SBOX.01	0.87	222-234	(-)	0.78	0.916
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	233-249	(-)	1	0.916
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	236-250	(-)	1	0.9
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	256-266	(+)	0.94	0.896
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	256-266	(-)	0.88	0.871
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	290-300	(-)	1	0.931
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	292-302	(-)	1	0.984
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	306-316	(+)	1	0.938
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	308-324	(-)	1	0.854
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	354-368	(+)	1	0.895
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	375-389	(-)	1	0.861
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	392-408	(-)	1	0.87
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	394-410	(+)	1	0.95
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.80	395-409	(-)	0.75	0.808
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	415-429	(+)	1	0.811
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	421-439	(-)	0.75	0.852
P\$WBXF	W Box family	P\$WRKY.01	0.92	426-442	(+)	1	0.939
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	431-447	(-)	0.76	0.782
P\$WBXF	W Box family	P\$WRKY.01	0.92	453-469	(+)	1	0.958
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	468-484	(-)	0.82	0.849
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	486-502	(+)	1	0.818

TABLE 3-continued

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	498-514	(-)	1	0.919
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	512-526	(-)	1	0.85
P\$WBXF	W Box family	P\$WRKY.01	0.92	533-549	(-)	1	0.966
P\$WBXF	W Box family	P\$WRKY.01	0.92	543-559	(+)	1	0.966
P\$WBXF	W Box family	P\$ERE.01	0.89	562-578	(+)	1	0.972
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	614-630	(+)	0.76	0.766
P\$GTBX	GT-box elements	P\$S1F.01	0.79	630-646	(+)	1	0.819
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	636-646	(-)	1	0.913
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	637-647	(+)	1	0.915
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	649-663	(+)	0.78	0.87
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	654-668	(-)	1	0.815
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	660-670	(-)	1	0.944
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	702-716	(-)	1	0.897
P\$GTBX	GT-box elements	P\$GT1.01	0.85	723-739	(-)	1	0.925
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	726-736	(-)	1	1
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	773-789	(+)	1	0.951
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	775-791	(+)	1	0.899
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	801-817	(-)	1	0.837
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	803-819	(-)	1	0.811
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	819-835	(-)	0.75	0.874
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	827-847	(-)	0.83	0.791
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	828-848	(+)	1	0.895
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	843-857	(-)	1	0.883
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	844-860	(-)	1	0.948
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	845-863	(+)	1	0.806
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	858-874	(+)	0.75	0.831
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	867-883	(+)	1	0.963
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	869-885	(+)	1	0.883
P\$RAV5	5'-part of bipartite RAV1 binding site	P\$RAV1-5.01	0.96	882-892	(+)	1	0.96
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	888-898	(-)	1	1
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	897-913	(+)	1	0.886
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	906-916	(+)	1	1
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	907-917	(-)	1	0.903
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	908-926	(-)	1	0.826
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	916-932	(-)	1	0.962
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXP.01	0.81	918-932	(-)	0.94	0.817
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	929-945	(-)	1	0.983
P\$GTBX	GT-box elements	P\$GT1.01	0.85	933-949	(+)	0.97	0.854
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	944-960	(+)	1	0.829

TABLE 3-continued

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	959-969	(+)	0.75	0.816
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	959-969	(-)	1	0.909
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	970-980	(+)	1	0.916
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	973-983	(+)	1	0.989
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	973-983	(-)	1	0.976
P\$IDDF	ID domain factors	P\$ID1.01	0.92	976-988	(+)	1	0.928
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	995-1011	(+)	1	0.96
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1008-1018	(+)	1	0.937
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	1012-1022	(-)	1	1
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	1029-1041	(-)	0.78	0.879
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1036-1054	(-)	1	0.822
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	1054-1064	(+)	1	0.99
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1054-1064	(-)	0.83	0.94
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	1066-1082	(+)	1	0.889
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	1086-1100	(+)	1	0.94
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1087-1103	(+)	0.89	0.927
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1088-1102	(+)	1	0.958
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1089-1105	(+)	1	0.971
P\$E2FF	E2F-homolog cell cycle regulators	P\$E2F.01	0.82	1117-1131	(-)	1	0.833
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	1146-1162	(+)	1	0.908
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1153-1169	(+)	1	0.8
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1170-1186	(-)	1	0.797
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1173-1191	(+)	1	0.813
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	1174-1194	(+)	1	0.9
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1189-1199	(+)	0.83	0.919
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1229-1245	(-)	0.76	0.763
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	1234-1250	(-)	0.94	0.88
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1241-1255	(+)	1	0.964
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1242-1258	(+)	1	0.967
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1265-1281	(-)	0.76	0.762
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	1265-1281	(+)	0.75	0.839
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1274-1284	(-)	1	0.928
P\$OCSE	Enhancer element first identified in the	P\$OCSL.01	0.69	1278-1298	(+)	0.77	0.732



TABLE 3-continued

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
	promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA						
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	1284-1302	(-)	0.86	0.963
P\$TALE	TALE (3-aa acid loop extension) class homeodomain proteins	P\$KN1_KIP.01	0.88	1289-1301	(-)	1	1
P\$AREF	Auxin response element	P\$SEBF.01	0.96	1292-1304	(+)	1	0.98
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.80	1295-1309	(-)	0.75	0.818
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1296-1312	(-)	1	0.776
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	1310-1326	(-)	0.94	0.876
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1319-1329	(+)	1	0.93
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1323-1339	(-)	1	0.881
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	1327-1337	(-)	1	0.936
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1338-1354	(+)	1	0.896
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1338-1356	(-)	1	0.819
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1345-1355	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1345-1355	(-)	1	0.998
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	1354-1364	(-)	1	0.916
O\$VTBP	Vertebrate TA-TA binding protein factor	O\$VTATA.01	0.90	1376-1392	(-)	1	0.949
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	1377-1391	(+)	1	0.952
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1379-1393	(-)	1	0.883
P\$IBOX	Plant I-Box sites	P\$IBOX.01	0.81	1399-1415	(-)	0.75	0.822
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	1417-1433	(-)	1	0.86
P\$IBOX	Plant I-Box sites	P\$IBOX.01	0.81	1419-1435	(-)	0.75	0.824
P\$WBXF	W Box family	P\$WRKY.01	0.92	1429-1445	(-)	1	0.958
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	1457-1473	(+)	0.82	0.798
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.02	0.77	1458-1482	(+)	0.75	0.786
P\$LFYB	LFY binding site	P\$LFY.01	0.93	1486-1498	(-)	0.91	0.987
P\$CAAT	CCAAT binding factors	P\$CAAT.01	0.97	1490-1498	(-)	1	0.982
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	1526-1540	(+)	1	0.833

TABLE 3-continued

Boxes and Motifs identified in the starting sequence of the VfSBP promoter							
p-VfSBP (nativ)							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1550-1560	(-)	1	0.93
P\$IDDF	ID domain factors	P\$ID1.01	0.92	1563-1575	(+)	1	0.952
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	1565-1579	(+)	0.75	0.845
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	1570-1586	(+)	1	0.846
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	1571-1587	(+)	1	0.988
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1572-1598	(-)	1	0.898
P\$MADS	MADS box proteins	P\$AGL3.01	0.83	1637-1657	(+)	1	0.851
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	1654-1670	(-)	1	0.909
P\$URNA	Upstream sequence element of U-snRNA genes	P\$USE.01	0.75	1659-1675	(+)	1	0.758
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	1671-1681	(-)	1	0.989
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$SHAHB4.01	0.87	1671-1681	(+)	1	0.955
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1677-1697	(+)	1	0.763
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	1682-1702	(-)	1	0.968
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	1685-1701	(-)	1	0.855
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	1696-1712	(-)	1	0.954
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	1696-1716	(-)	1	0.963
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1696-1716	(-)	0.96	0.826
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	1698-1714	(-)	0.95	0.824
P\$DPBF	Dc3 promoter binding factors	P\$DPBF.01	0.89	1700-1710	(+)	1	0.943
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1701-1727	(-)	1	0.887
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	1708-1734	(+)	1	0.871
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	1727-1743	(+)	1	0.85
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.02	0.77	1740-1764	(+)	1	0.786
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$EMBP1.01	0.84	1747-1767	(-)	1	0.84
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	1750-1766	(-)	1	0.831
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1756-1772	(+)	1	0.963
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	1765-1781	(-)	1	0.781

TABLE 4

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.90	12-28	(+)	1	0.918
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	25-35	(-)	1	0.914
P\$GAGA	GAGA elements	P\$BPC.01	1.00	25-49	(-)	1	1
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	26-36	(+)	1	0.914
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	80-106	(-)	1	0.805
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	85-101	(-)	1	0.843
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	101-117	(-)	1	0.883
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$HBP1B.01	0.83	138-158	(+)	1	0.834
P\$WBXF	W Box family	P\$ERE.01	0.89	154-170	(-)	1	0.935
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	165-181	(-)	0.78	0.788
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$TANAC69.01	0.68	173-195	(-)	0.81	0.728
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	174-194	(-)	0.98	0.856
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	175-195	(+)	0.98	0.844
P\$TCPF	DNA-binding proteins with the plant specific TCP-domain	P\$ATTCP20.01	0.94	189-201	(+)	1	0.968
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	194-210	(-)	0.89	0.795
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	198-208	(+)	0.83	0.936
P\$EINL	Ethylen insensitive 3 like factors	P\$TEIL.01	0.92	215-223	(-)	0.96	0.924
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$HBP1A.01	0.88	217-237	(-)	1	0.908
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	218-238	(+)	1	0.963
P\$GTBX	GT-box elements	P\$S1F.01	0.79	218-234	(+)	1	0.821
P\$ABRE	ABA response elements	P\$ABF1.03	0.82	219-235	(+)	1	0.825
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	221-245	(-)	1	0.803
P\$CE1F	Coupling element 1 binding factors	P\$SBOX.01	0.87	222-234	(-)	0.78	0.916
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	233-249	(-)	1	0.939
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	245-261	(-)	1	0.963
P\$MYBS	MYB proteins with single DNA binding repeat	P\$HVMCB1.01	0.93	248-264	(+)	1	0.957

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	256-266	(+)	0.94	0.896
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	256-266	(-)	0.88	0.871
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	260-276	(+)	1	0.819
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	290-300	(-)	1	0.931
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	292-302	(-)	1	0.984
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	293-303	(+)	1	0.915
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	306-316	(+)	1	0.938
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	308-324	(-)	1	0.854
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	319-335	(+)	1	0.87
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	322-332	(+)	1	0.969
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	345-365	(+)	0.85	0.825
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	354-368	(+)	1	0.895
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	375-389	(-)	1	0.861
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	392-408	(-)	1	0.87
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	394-410	(+)	1	0.95
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.80	395-409	(-)	0.75	0.808
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	402-416	(-)	1	0.929
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	404-418	(+)	1	0.871
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	407-417	(-)	1	0.901
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	411-421	(+)	1	0.916
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	415-429	(+)	1	0.811
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	421-439	(-)	0.75	0.849
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	431-447	(-)	0.76	0.782
P\$WBXF	W Box family	P\$WRKY.01	0.92	453-469	(+)	1	0.958
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	468-484	(-)	0.82	0.849
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	486-502	(+)	1	0.818
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	498-514	(-)	1	0.919
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	512-526	(-)	1	0.824

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	525-539	(-)	0.75	0.815
P\$WBXF	W Box family	P\$WRKY.01	0.92	533-549	(-)	1	0.966
P\$WBXF	W Box family	P\$WRKY.01	0.92	543-559	(+)	1	0.966
P\$WBXF	W Box family	P\$ERE.01	0.89	562-578	(+)	1	0.972
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	614-630	(+)	0.76	0.766
P\$GTBX	GT-box elements	P\$S1F.01	0.79	630-646	(+)	1	0.819
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	636-646	(-)	1	0.913
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	637-647	(+)	1	0.921
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	640-656	(-)	1	0.918
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	649-663	(+)	0.78	0.87
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	654-668	(-)	1	0.815
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	660-670	(-)	1	0.944
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	691-721	(-)	1	0.789
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	702-716	(-)	1	0.897
P\$GTBX	GT-box elements	P\$GT1.01	0.85	723-739	(-)	1	0.925
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	726-736	(-)	1	1
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	731-749	(+)	1	0.855
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$ICE.01	0.95	734-752	(+)	0.95	0.961
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	773-789	(+)	1	0.951
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	775-791	(+)	1	0.899
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	801-817	(-)	1	0.837
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	803-819	(-)	1	0.811
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	814-830	(-)	1	0.869
P\$GTBX	GT-box elements	P\$GT1.01	0.85	815-831	(-)	0.97	0.854
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	819-835	(-)	0.75	0.874
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	828-848	(+)	1	0.857
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	843-857	(-)	1	0.883
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	844-860	(-)	1	0.948
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	845-863	(+)	1	0.806
P\$MYBL	MYB-like proteins	P\$CARE.01	0.83	849-865	(-)	1	0.876
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	869-885	(+)	1	0.883
P\$RAV5	5'-part of bipartite RAV1 binding site	P\$RAV1-5.01	0.96	882-892	(+)	1	0.96
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	884-900	(-)	0.85	0.853
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	888-898	(-)	1	1
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	895-911	(+)	1	0.962
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	897-913	(+)	1	0.883
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	906-916	(+)	1	1
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	907-917	(-)	1	0.903

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	908-926	(-)	1	0.826
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	916-932	(-)	1	0.962
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXP.01	0.81	918-932	(-)	0.94	0.817
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	931-943	(-)	1	0.889
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	948-964	(+)	1	0.908
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	959-969	(+)	0.75	0.816
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	959-969	(-)	1	0.909
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	970-980	(+)	1	0.916
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	973-983	(+)	1	0.989
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	973-983	(-)	1	0.976
P\$IDDF	ID domain factors	P\$ID1.01	0.92	976-988	(+)	1	0.928
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	985-995	(+)	1	0.916
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	985-1001	(+)	1	0.891
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	986-1002	(-)	1	0.877
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	992-1002	(-)	1	0.916
P\$IIBOX	Plant I-Box sites	P\$GATA.01	0.93	995-1011	(+)	1	0.935
P\$LEGB	Legumin Box family	P\$LEGB.01	0.65	998-1024	(+)	0.75	0.676
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1008-1018	(+)	1	0.937
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	1012-1022	(-)	1	1
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	1022-1038	(-)	1	0.925
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	1029-1041	(-)	0.78	0.879
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1036-1054	(-)	1	0.83
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.90	1054-1064	(+)	1	0.99
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1054-1064	(-)	0.83	0.94
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	1066-1082	(+)	1	0.889
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.90	1086-1100	(+)	1	0.94
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1087-1103	(+)	0.89	0.927
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1088-1102	(+)	1	0.958
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1089-1105	(+)	1	0.971
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF3.01	0.99	1098-1114	(+)	1	0.995
P\$E2FF	E2F-homolog cell cycle regulators	P\$E2F.01	0.82	1117-1131	(-)	1	0.833
P\$SPF1	Sweet potato DNA-binding factor with two	P\$SP8BF.01	0.87	1130-1142	(+)	1	0.881

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
	WRKY-domains						
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	1146-1162	(+)	1	0.873
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1170-1186	(-)	1	0.797
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1173-1191	(+)	1	0.813
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	1174-1194	(+)	1	0.9
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1189-1199	(+)	0.83	0.919
P\$IDDF	ID domain factors	P\$ID1.01	0.92	1205-1217	(-)	1	0.97
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1229-1245	(-)	0.76	0.763
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	1234-1250	(-)	0.94	0.88
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1241-1255	(+)	1	0.964
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1242-1258	(+)	1	0.967
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1265-1281	(-)	0.76	0.762
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	1265-1281	(+)	0.75	0.839
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1274-1284	(-)	1	0.928
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1277-1291	(+)	1	0.908
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1278-1294	(+)	1	0.918
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1278-1298	(+)	0.77	0.712
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$MYCRS.01	0.93	1284-1302	(-)	0.86	0.933
P\$TALE	TALE (3-aa acid loop extension) class homeodomain proteins	P\$KN1_KIP.01	0.88	1289-1301	(-)	1	1
P\$AREF	Auxin response element	P\$SEBF.01	0.96	1292-1304	(+)	1	0.98
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.80	1295-1309	(-)	0.75	0.803
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	1296-1312	(-)	1	0.797
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	1310-1326	(-)	0.94	0.876
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1319-1329	(+)	1	0.93
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1323-1339	(-)	1	0.833
P\$LREM	Light responsive element motif, not modulated by different	P\$RAP22.01	0.85	1327-1337	(-)	1	0.936

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

P- VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
	light qualities						
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1328-1344	(+)	1	0.939
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1334-1352	(+)	1	0.816
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1335-1345	(-)	0.83	0.904
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1335-1345	(+)	1	0.998
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1338-1354	(+)	1	0.896
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1338-1356	(-)	1	0.819
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1345-1355	(+)	0.83	0.902
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1345-1355	(-)	1	0.998
P\$AGP1	Plant GATA-type zinc finger protein	P\$AGP1.01	0.91	1354-1364	(-)	1	0.916
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1365-1375	(-)	1	0.896
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1376-1392	(-)	1	0.949
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	1377-1391	(+)	1	0.952
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	1379-1393	(-)	1	0.883
P\$IDDF	ID domain factors	P\$ID1.01	0.92	1387-1399	(+)	1	0.926
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	1389-1405	(+)	1	0.939
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1392-1402	(+)	1	0.943
P\$IBOX	Plant I-Box sites	P\$IBOX.01	0.81	1399-1415	(-)	0.75	0.822
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	1410-1426	(+)	1	0.875
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	1412-1424	(+)	1	0.91
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	1417-1433	(-)	1	0.847
P\$IBOX	Plant I-Box sites	P\$IBOX.01	0.81	1419-1435	(-)	0.75	0.824
P\$WBXF	W Box family	P\$WRKY.01	0.92	1429-1445	(-)	1	0.958
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	1457-1473	(+)	0.82	0.798
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.02	0.77	1458-1482	(+)	0.75	0.786
P\$LFYB	LFY binding site	P\$LFY.01	0.93	1486-1498	(-)	0.91	0.987
P\$CAAT	CCAAT binding factors	P\$CAAT.01	0.97	1490-1498	(-)	1	0.982
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	1526-1540	(+)	1	0.833
P\$GTBX	GT-box elements	P\$GT1.01	0.85	1536-1552	(-)	0.84	0.869
P\$WBXF	W Box family	P\$ERE.01	0.89	1537-1553	(+)	1	0.9
P\$SPF1	Sweet potato DNA-binding factor with two WRKY-domains	P\$SP8BF.01	0.87	1546-1558	(+)	1	0.919
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.90	1550-1560	(-)	1	0.93
P\$LREM	Light responsive element motif, not modulated	P\$RAP22.01	0.85	1555-1565	(-)	1	0.882



TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

p-VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
	by different light qualities						
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	1559-1569	(-)	0.8	0.855
P\$GARP	Myb-related DNA binding proteins (Golden2, ARR, Psr)	P\$ARR10.01	0.97	1560-1568	(+)	1	0.97
P\$IDDF	ID domain factors	P\$ID1.01	0.92	1563-1575	(+)	1	0.952
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	1565-1579	(+)	0.75	0.845
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	1570-1586	(+)	1	0.846
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	1571-1587	(+)	1	0.988
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1572-1598	(-)	1	0.898
P\$NCS2	Nodulin consensus sequence 2	P\$NCS2.01	0.79	1610-1624	(+)	1	0.867
P\$MADS	MADS box proteins	P\$AGL3.01	0.83	1637-1657	(+)	1	0.851
P\$GTBX	GT-box elements	P\$GT3A.01	0.83	1652-1668	(-)	1	0.854
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	1654-1670	(-)	1	0.971
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1671-1681	(+)	1	0.934
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1677-1697	(+)	1	0.763
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	1682-1702	(-)	1	0.968
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	1685-1701	(-)	1	0.855
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	1696-1712	(-)	1	0.954
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$GBF1.01	0.94	1696-1716	(-)	1	0.963
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1696-1716	(-)	0.84	0.799
P\$DPBF	Dc3 promoter binding factors	P\$DPBF.01	0.89	1700-1710	(+)	1	0.943
P\$EREF	Ethylen response element factors	P\$ANT.01	0.81	1701-1717	(+)	1	0.862
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1701-1727	(-)	1	0.925
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1704-1730	(+)	1	0.967
P\$LEGB	Legumin Box family	P\$IDE1.01	0.77	1708-1734	(+)	1	0.888
P\$MADS	MADS box proteins	P\$MADS.01	0.75	1722-1742	(+)	1	0.758
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	1727-1743	(+)	1	0.861
P\$URNA	Upstream sequence element of U-snRNA genes	P\$USE.01	0.75	1731-1747	(+)	1	0.77

TABLE 4-continued

Boxes and Motifs identified in the permuted sequence of the VfsBP promoter. Preferably associated boxes are annotated in line 8, 14, 26, 56, 58, 59, 66, 121, 144, 148, 158, 185, 200, 201, 211, 215, 218, 219, 220, 225, 226, 228 of tables 3 and 4. Essential boxes are annotated in line 130, 132 and 146 of tables 3 and 4.

p-VfsBP_perm							
Family	Further Family Information	Matrix	Opt.	Position from-to	Strand	Core sim.	Matrix sim.
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.02	0.77	1740-1764	(+)	1	0.79
P\$GBOX	Plant G-box/C-box bZIP proteins	P\$EMBP1.01	0.84	1747-1767	(-)	1	0.84
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	1750-1766	(-)	1	0.831
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.90	1756-1772	(+)	1	0.957
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	1765-1781	(-)	1	0.781

### 1.2 Vector Construction

Using the Multisite Gateway System (Invitrogen, Carlsbad, Calif., USA), promoter::reporter-gene cassettes were assembled into binary constructs for plant transformation. beta-Glucuronidase (GUS) or uidA gene which encodes an enzyme for which various chromogenic substrates are known, was utilized as reporter protein for determining the expression features of the permuted p-PvArc5\_perm (SEQ ID NO2) and p-VfsBP\_perm (SEQ ID NO4) promoter sequences. The DNA fragments representing promoters p-PvArc5\_perm (SEQ ID NO2) and p-VfsBP\_perm (SEQ ID NO4) were generated by gene synthesis. Endonucleolytic restriction sites suitable for cloning the promoter fragments into beta-Glucuronidase reporter gene cassettes were included in the synthesis. The p-PvArc5\_perm (SEQ ID NO2) promoter was cloned into a pENTR/A vector harboring the beta-Glucuronidase reporter gene c-GUS (with the prefix c- denoting coding sequence) followed by the t-PvArc (with the prefix t- denoting terminator) transcription terminator sequence using restriction endonucleases FseI and NcoI, yielding construct LJB2012. Similarly, the p-VfsBP\_perm (SEQ ID NO4) promoter was cloned into a pENTR/B vector harboring the beta-Glucuronidase reporter gene c-GUS followed by the t-StCatpA transcriptional terminator sequence using restriction endonucleases FseI and NcoI, yielding construct LJB2007.

The complementary pENTR vectors without any expression cassettes were constructed by introduction of a multiple cloning site via KpnI and HindIII restriction sites. By performing a site specific recombination (LR-reaction), the created pENTR/A, pENTR/B and pENTR/C were combined with the pSUN destination vector (pSUN derivative) according to the manufacturers (Invitrogen, Carlsbad, Calif., USA) Multisite Gateway manual. The reactions yielded a binary vector with the p-PvArc5\_perm (SEQ ID NO2) promoter, the beta-Glucuronidase coding sequence c-GUS and the t-PvArc terminator, for which the full construct sequence is given (SEQ ID NO7). Accordingly, a binary vector with the p-VfsBP\_perm (SEQ ID NO4) promoter, the beta-Glucuronidase reporter gene and the t-StCatpA terminator for which the full construct sequence is given (SEQ ID NO8). The resulting plant transformation vectors are summarized in table 5:

TABLE 5

Plant expression vectors for <i>B. napus</i> transformation		
plant expression vector	Composition of the expression cassette Promoter::reporter gene::terminator	SEQ ID NO
LJB2045	p-PvArc5_perm::c-GUS::t-PvArc	7
LJB2043	p-VfsBP_perm::c-GUS::t-StCatpA	8

### 1.3 Generation of Transgenic Rapeseed Plants

(amended protocol according to Moloney et al., 1992, Plant Cell Reports, 8: 238-242).

In preparation for the generation of transgenic rapeseed plants, the binary vectors were transformed into *Agrobacterium tumefaciens* C58C1:pGV2260 (Deblaere et al., 1985, Nucl. Acids. Res. 13: 4777-4788). A 1:50 dilution of an overnight culture of Agrobacteria harboring the respective binary construct was grown in Murashige-Skoog Medium (Murashige and Skoog, 1962, Physiol. Plant 15, 473) supplemented with 3% saccharose (3MS-Medium). For the transformation of rapeseed plants, petioles or hypocotyledons of sterile plants were incubated with a 1:50 *Agrobacterium* solution for 5-10 minutes followed by a three-day co-incubation in darkness at 25° C. on 3 MS. Medium supplemented with 0.8% bacto-agar. After three days, the explants were transferred to MS-medium containing 500 mg/l Claforan (Cefotaxime-Sodium), 100 nM Imazetapyr, 20 microM Benzylaminopurin (BAP) and 1.6 g/l Glucose in a 16 h light/8 h darkness light regime, which was repeated in weekly periods. Growing shoots were transferred to MS-Medium containing 2% saccharose, 250 mg/l Claforan and 0.8% Bacto-agar. After 3 weeks, the growth hormone 2-Indolbutyl acid was added to the medium to promote root formation. Shoots were transferred to soil following root development, grown for two weeks in a growth chamber and grown to maturity in greenhouse conditions.

#### Example 2: Expression Profile of the p-PvArc5\_Perm and p-VfsBP\_Perm Gene Control Elements

To demonstrate and analyze the transcription regulating properties of a promoter, it is useful to operably link the promoter or its fragments to a reporter gene, which can be employed to monitor its expression both qualitatively and quantitatively. Preferably bacterial  $\beta$ -glucuronidase is used

(Jefferson 1987).  $\beta$ -glucuronidase activity can be monitored in planta with chromogenic substrates such as 5-bromo-4-Chloro- $\beta$ -indolyl-R-D-glucuronic acid during corresponding activity assays (Jefferson 1987). For determination of promoter activity and tissue specificity, plant tissue is dissected, stained and analyzed as described (e.g., Bäumlein 1991).

The regenerated transgenic T0 rapeseed plants harboring single or double insertions of the transgene deriving from constructs LJB2043 or LJB2045 were used for reporter gene analysis. Table 6 summarizes the reporter gene activity observed in plants harboring transgenes containing SEQ ID NO2 and SEQ ID NO4 in constructs LJB2043 and LJB2045, respectively:

TABLE 6

beta-Glucuronidase reporter gene activity in selected rapeseed plants harboring transgenes with SEQ ID NO2 (p-PvArc5-perm) and SEQ ID NO4 (p-VfSBP-perm) compared to the GUS expression derived from the respective starting sequence in rapeseed (p-VfSBP) or <i>Phaseolus</i> and <i>Arabidopsis</i> plants (p-PvArc5).				
Tissue	LJB2043 p-VfSBP-perm	p-VfSBP	LJB2045 p-PvArc5__perm	p-PvArc5*
leaves	negative	negative	negative	negative
stem	negative	negative	negative	negative
roots	negative	negative	negative	negative
flower	negative	negative	negative	negative
silique (without seed)	negative	not analyzed	negative	not assayed
embryo (early)	weak	weak	strong	strong, no
embryo (young)	weak	weak	strong	seperate
embryo (medium)	strong	strong	strong	analyses of different stages
embryo (mature)	strong	strong	strong	strong
seed shell	weak	not analyzed	strong	strong

\*expression in *Phaseolus* and *Arabidopsis* according to Goossens et al.

The gene expression activity conferred by p-PvArc5\_perm and p-VfSBP\_perm is shown exemplary in FIG. 1 (p-PvArc5\_perm) and in FIG. 2 (P-VfSBP\_perm).

General results for SEQ ID NO2: Strong GUS expression was detected in all stages of embryo development and in seed shells. No activity was found in other tissues analyzed.

General results for SEQ ID NO4: Weak GUS expression was detected in early and young embryo stages, strong GUS expression could be observed in medium and mature embryos. Weak expression was monitored in seed shells. No activity was found in other tissues investigated.

### Example 3

#### 3.1 Random Permutation of the Promoter Sequence

Using publicly available data, a promoter showing seed specific expression in plants was selected for analyzing the effects of sequence permutation in periodic intervals throughout the full length of the promoter DNA sequence. The wild type sequences of the *Brassica napus* p-BnNapin promoter was analyzed and annotated for the occurrence of cis-regulatory elements using available literature data (Ellerström et al., Ericson et al., Ezcurra et al.). In the following, the DNA sequence of the promoter was permuted in the region of -1000 to +1 nucleotides with the following criteria to yield p-BnNapin\_perm (SEQ ID NO6): DNA permutation was conducted in a way to not affect cis regulatory elements which have been proven previously to be essential for seed specific gene expression and motives essential for gene expression. The remaining promoter sequence was ran-

domly permuted resulting in a promoter sequence with an overall nucleotide homology of 75% to the initial p-BnNapin sequence

#### 3.2 Vector Construction

Using the Multisite Gateway System (Invitrogen, Carlsbad, Calif., USA), promoter::reporter-gene cassettes were assembled into binary constructs for plant transformation. Beta-Glucuronidase (GUS) or uidA gene which encodes an enzyme for which various chromogenic substrates are known, was utilized as reporter protein for determining the expression features of the permuted p-BnNapin\_perm (SEQ ID NO6) promoter sequences.

The DNA fragments representing promoter p-BnNapin\_perm was generated by gene synthesis. Endonucleolytic restriction sites suitable for cloning the promoter fragment into a beta-Glucuronidase reporter gene cassette was included in the synthesis. p-BnNapin\_perm (SEQ ID NO6) promoter was cloned into a pENTR/A vector harboring the beta-Glucuronidase reporter gene c-GUS (with the prefix c- denoting coding sequence) followed by the t-nos transcription terminator sequence using restriction endonucleases BamHI and NcoI, yielding pENTR/A LLL1168.

A 1138 bp DNA fragment representing the native promoter p-BnNapin (SEQ ID NO5) was generated by PCR with the following primers.

Loy963

SEQ ID NO11

GATATAGGTACCTCTTCATCGGTGATTGATTCCT

Loy964

SEQ ID NO12

GATATACCATGGTCGTATGTTTTTAATCTGTTTG

Endonucleolytic restriction sites suitable for cloning the promoter fragment into a beta-Glucuronidase reporter gene cassette were included in the primers. p-BnNapin (SEQ ID NO5) promoter was cloned into a pENTR/A vector harboring the beta-Glucuronidase reporter gene c-GUS (with the prefix c- denoting coding sequence) followed by the t-nos transcription terminator sequence using restriction endonucleases KpnI and NcoI, yielding pENTR/A LLL1166.

By performing a site specific recombination (LR-reaction), the newly created pENTRs/A LLL1168 and LLL1166, were combined with pENTR/B and pENTR/C and the pSUN destination vector (pSUN derivative) according to the manufacturers (Invitrogen, Carlsbad, Calif., USA) Multisite Gateway manual. The reaction yielded binary vector LLL 1184 with the p-BnNapin\_perm (SEQ ID NO6) promoter, the beta-Glucuronidase coding sequence c-GUS and the t-nos terminator, and binary vector LLL 1176 with the native p-BnNapin (SEQ ID NO5) promoter, the beta-Glucuronidase coding sequence c-GUS and the t-nos terminator. For both vectors the full construct sequence is given (SEQ ID NO9 and 10). The resulting plant transformation vectors are shown in table 7:

TABLE 7

Plant expression vectors for <i>A. thaliana</i> transformation		
plant expression vector	Composition of the expression cassette Promoter::reporter gene::terminator	SEQ ID NO
LLL1184	p-BnNapin_perm::c-GUS::t-nos	9
LLL1176	p-BnNapin::c-GUS::t-nos	10

#### 3.3 Generation of *Arabidopsis thaliana* Plants

*A. thaliana* plants were grown in soil until they flowered. *Agrobacterium tumefaciens* (strain C58C1 [pMP90]) transformed with the construct of interest was grown in 500 mL

in liquid YEB medium (5 g/L Beef extract, 1 g/L Yeast Extract (Duchefa), 5 g/L Peptone (Duchefa), 5 g/L sucrose (Duchefa), 0.49 g/L MgSO<sub>4</sub> (Merck)) until the culture reached an OD<sub>600</sub> 0.8-1.0. The bacterial cells were harvested by centrifugation (15 minutes, 5,000 rpm) and resuspended in 500 mL infiltration solution (5% sucrose, 0.05% SILWET L-77 [distributed by Lehle seeds, Cat.No. VIS-02]). Flowering plants were dipped for 10-20 seconds into the *Agrobacterium* solution. Afterwards the plants were kept in the dark for one day and then in the greenhouse until seeds could be harvested. Transgenic seeds were selected on soil by spraying the seeds directly after sowing with a solution of 0.016 g/l Imazamox. After 12 to 14 days surviving plants were transferred to pots and grown in the greenhouse.

#### Example 4: Expression Profile of the Native p-Bn-Napin and the p-BnNapin\_Perm Gene Control Elements

To demonstrate and analyze the transcription regulating properties of a promoter, it is useful to operably link the promoter or its fragments to a reporter gene, which can be employed to monitor its expression both qualitatively and quantitatively. Preferably bacterial  $\beta$ -glucuronidase is used (Jefferson 1987).  $\beta$ -glucuronidase activity can be monitored in planta with chromogenic substrates such as 5-bromo-4-Chloro-3-indolyl- $\beta$ -D-glucuronic acid during corresponding activity assays (Jefferson 1987). For determination of promoter activity and tissue specificity, plant tissue is dissected, stained and analyzed as described (e.g., Bäumlein 1991).

The regenerated transgenic T0 *Arabidopsis* plants harboring single or double insertions of the transgene deriving from constructs LLL1184 (SEQ ID NO9) and constructs LLL1176 (SEQ ID NO10) were used for reporter gene analysis. Table 8 summarizes the reporter gene activity observed in plants harboring transgenes containing SEQ ID NO9 and SEQ ID NO10 in constructs LLL1184 and LLL1176, respectively:

TABLE 8

beta-Glucuronidase reporter gene activity in selected <i>Arabidopsis</i> plants harboring transgenes with SEQ ID NO 9 or 10 respectively.		
Tissue	LLL1176	LLL1184
leaves	negative	negative
Stem	negative	negative
Roots	negative	negative
Flower	negative	negative
Silique	weak	weak
Embryo (medium)	strong	strong
Embryo (mature)	strong	strong

The gene expression activity conferred by pBn-Napin and p-BNnapin\_perm is shown exemplary in FIG. 3 (p-Bn\_napin SEQ ID NO5, p-BnNapin\_perm SEQ ID NO6)

General results for SEQ ID NO5 and 6: For both promoters pBn-Napin and p-BNnapin\_perm strong GUS expression was detected in medium to mature stages of embryo development. Weak expression was monitored in seed shells and in siliques. No activity was found in other tissues analyzed.

#### Example 5: Directed Permutation of a Constitutive Promoter Sequence

Using publicly available data, one promoters showing constitutive expression in plants was selected (de Pater, B. S., van der Mark, F., Rueb, S., Katagiri, F., Chua, N. H., Schilperoort, R. A. and Hensgens, L. A. (1992) The promoter of the rice gene GOS2 is active in various different monocot tissues and binds rice nuclear factor ASF-1 Plant J. 2 (6)) for analyzing the effects of sequence permutation in periodic intervals throughout the full length of the promoter DNA sequence. The wildtype or starting sequence of the *Oryza sativa* p-GOS2 (SEQ ID NO 13) (with the prefix p-denoting promoter) promoter was analyzed and annotated for the occurrence of motives, boxes, cis-regulatory elements using e.g. the GEMS Launcher Software (www.genomatix.de) as described above in example 1.

The promoter p-Gos2 encompasses a 5'UTR sequence with an internal intron. To ensure correct splicing of the intron after permutation, splice sites and putative branching point were not altered. No nucleotide exchanges were introduced into sequences 10 bp up- and downstream of the splice site (5' GT; 3' CAG) and "TNA" sequence elements within the last 100 base pairs of the original p-Gos2 were preserved after permutation.

In the following, the DNA sequence of the promoter was permuted according to the method of the invention to yield p-GOS2\_perm1 and p-GOS2\_perm2 respectively (SEQ ID NO 14 and 15).

The list of motives, boxes, cis regulatory elements in the p-GOS2 promoters before and after the permutation are shown in Table 9 for the starting sequence of p-GOS2, Table 10 for the p-GOS2\_perm1 (SEQ ID NO 14) and Table 11 for the p-GOS2\_perm2 sequence (SEQ ID NO 15).

Empty lines resemble motives, boxes, cis regulatory elements not found in one sequence but present in the corresponding sequence, hence, motives, boxes, cis regulatory elements that were deleted from the starting sequence or that were introduced into the permuted sequence.

TABLE 9

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter							
p-GOS2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	Position	Position	sim.	sim.
				from-to	—	—	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	6	16	1	0.857
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	15	29	1	0.832
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	29	45	1	0.927
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	33	49	1	0.897
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	35	55	0.79	0.82

TABLE 9-continued

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter							
p-GOS2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	Position	Position	sim.	sim.
				from-to	—	—	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$IDEF2.01	0.96	48	60	1	0.96
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	48	64	1	0.954
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	60	74	1	0.883
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	61	77	1	0.961
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	65	75	0.97	0.94
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	69	85	1	0.842
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	71	87	0.89	0.921
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	74	90	1	0.832
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	75	91	1	0.876
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	76	92	0.75	0.781
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	77	93	0.76	0.835
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXL.01	0.8	118	132	0.77	0.841
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	126	142	1	0.99
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	149	165	1	0.989
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	170	192	0.81	0.712
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	187	203	1	0.922
P\$E2FF	E2F-homolog cell cycle regulators	P\$E2F.01	0.82	193	207	1	0.829
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	200	210	0.97	0.945
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	207	217	0.83	0.903
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	207	217	1	0.967
P\$CNAC	Calcium regulated NAC-factors	P\$CBNAC.02	0.85	215	235	1	0.947
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	217	233	1	0.944
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	216	236	1	0.722
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	222	238	1	0.979
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	246	262	1	0.901
P\$STKM	Storekeeper motif	P\$STK.01	0.85	251	265	1	0.85
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	254	264	0.83	0.904
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	254	264	1	0.998
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	284	300	1	0.757
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	297	311	1	0.953
P\$LFYB	LFY binding site	P\$LFY.01	0.93	318	330	0.91	0.945
P\$GAGA	GAGA elements	P\$BPC.01	1	329	353	1	1
P\$CCAF	Circadian control factors	P\$EE.01	0.84	335	349	0.75	0.865
P\$GAGA	GAGA elements	P\$BPC.01	1	331	355	1	1
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	337	351	1	0.968
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	341	357	1	0.875
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	345	365	1	0.925
P\$CCAF	Circadian control factors	P\$EE.01	0.84	363	377	1	0.925
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	383	399	1	0.895
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	388	406	1	0.785
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	397	407	1	0.902

TABLE 9-continued

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter								
Family	Further Family Information	Matrix	Opt.	p-GOS2		Position	Core	Matrix
				from	to	Position	sim.	sim.
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	395	411	1	0.889	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	396	412	1	0.844	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	398	412	1	0.892	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	397	413	0.75	0.781	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	400	410	1	0.902	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	402	418	0.75	0.781	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	405	421	1	0.983	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	408	422	1	0.917	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSTF.01	0.73	426	446	1	0.784	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	440	450	1	0.926	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	444	454	1	1	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	447	463	1	0.819	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	472	482	1	0.984	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	481	497	1	0.922	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	482	498	1	0.994	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	482	498	1	0.9	
P\$WBXF	W Box family	P\$WRKY11.01	0.94	493	509	1	0.963	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	504	514	1	0.994	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	509	525	1	0.961	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	515	525	1	0.948	
P\$GTBX	GT-box elements	P\$S1F.01	0.79	518	534	0.75	0.793	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	527	537	1	0.897	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	525	541	0.75	0.825	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	539	555	0.75	0.782	
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	568	592	0.75	0.772	
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	591	607	1	0.837	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	599	607	1	0.867	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	629	645	1	0.89	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	631	647	0.8	0.783	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	638	654	1	0.877	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	649	663	1	0.899	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	687	703	1	0.987	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	689	705	1	0.888	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	695	705	1	0.929	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	694	708	1	0.954	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	701	711	1	1	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	699	715	0.75	0.822	
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	711	725	1	0.929	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.9	716	726	0.79	0.901	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	716	726	1	0.998	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	716	732	1	0.893	

TABLE 9-continued

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter								
Family	Further Family Information	Matrix	Opt.	p-GOS2		Position	Core	Matrix
				from	to	Position	sim.	sim.
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	715	733	1	0.856	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	718	734	0.76	0.762	
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	718	734	1	0.833	
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	733	747	1	0.924	
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	744	760	0.78	0.834	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	754	770	0.75	0.831	
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	756	770	0.75	0.869	
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$OSBHLH66.01	0.85	789	807	1	0.851	
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	793	809	1	0.998	
P\$URNA	Upstream sequence element of U-snRNA genes	P\$USE.01	0.75	812	828	0.75	0.797	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	812	832	1	0.895	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	813	833	0.92	0.911	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	872	882	0.81	0.888	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	879	889	1	0.896	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	880	894	1	0.877	
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	900	916	0.95	0.968	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	909	925	1	0.905	
P\$MYBL	MYB-like proteins	P\$AS1_AS2_I.01	0.99	911	927	1	1	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	981	991	1	0.893	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	982	996	1	0.951	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	982	998	1	0.884	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	983	999	1	0.955	
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	1006	1026	0.83	0.793	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1008	1024	0.78	0.811	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1010	1024	1	0.91	
P\$CGCG	Calmodulin binding/CGCG box binding proteins	P\$ATSR1.01	0.84	1051	1067	1	0.859	
P\$ABRE	ABA response elements	P\$ABF1.01	0.79	1053	1069	1	0.837	
P\$CE3S	Coupling element 3 sequence	P\$CE3.01	0.77	1052	1070	1	0.893	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC092.01	0.92	1055	1067	1	0.927	
P\$DPBF	De3 promoter binding factors	P\$DPBF.01	0.89	1057	1067	1	0.908	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1059	1089	1	0.806	
O\$MTEN	Core promoter motif ten elements	O\$HMTE.01	0.88	1072	1092	0.96	0.94	
P\$DREB	Dehydration responsive element binding factors	P\$HVDRF1.01	0.89	1079	1093	1	0.922	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1077	1107	1	0.805	
O\$MTEN	Core promoter motif ten elements	O\$DMTE.01	0.77	1097	1117	0.84	0.805	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.02	0.87	1135	1151	1	0.915	
P\$SALT	Salt/drought responsive elements	P\$ALFIN1.02	0.95	1136	1150	1	0.954	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	1179	1195	1	0.882	
P\$SBPD	SBP-domain proteins	P\$SBP.01	0.88	1199	1215	1	0.912	
P\$PALA	Conserved box A in PAL and 4CL gene promoters	P\$PALBOXA.01	0.84	1201	1219	1	0.863	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1230	1246	1	0.833	

TABLE 9-continued

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter							
Family	Further Family Information	Matrix	Opt.	Position		Core	Matrix
				Position	from-to	sim.	sim.
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1244	1254	1	0.867
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	1248	1268	0.97	0.828
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1262	1278	1	0.953
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	1278	1294	1	0.864
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1277	1303	1	0.871
P\$MYBS	MYB proteins with single DNA binding repeat	P\$OSMYBS.01	0.82	1343	1359	0.75	0.822
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1349	1359	0.97	0.955
P\$STKM	Storekeeper motif	P\$STK.01	0.85	1355	1369	1	0.95
P\$GTBX	GT-box elements	P\$GT1.01	0.85	1403	1419	0.97	0.865
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1439	1455	0.75	0.797
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1437	1457	0.77	0.745
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1478	1494	1	0.764
P\$WBXF	W Box family	P\$WRKY.01	0.92	1488	1504	1	0.94
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1491	1511	0.96	0.858
P\$MYBS	MYB proteins with single DNA binding repeat	P\$HVMCB1.01	0.93	1498	1514	1	0.934
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	1509	1525	0.75	0.837
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	1551	1565	1	0.802
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	1558	1574	1	0.883
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569	1579	0.83	0.904
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569	1579	0.94	0.978
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1609	1625	0.75	0.781
PSLREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	1613	1623	1	0.966
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1617	1637	0.84	0.812
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	1625	1647	0.9	0.775
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC019.01	0.94	1632	1644	0.95	0.968
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1642	1658	1	0.917
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	1644	1660	1	0.864
P\$MYBL	MYB-like proteins	P\$MYBPH3.01	0.8	1647	1663	1	0.938
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	1694	1710	1	1
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1703	1719	0.86	0.757
P\$CCAF	Circadian control factors	P\$EE.01	0.84	1719	1733	1	0.955
P\$MADS	MADS box proteins	P\$AG.01	0.8	1717	1737	0.9	0.816
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1732	1748	1	0.967
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1749	1759	1	0.957
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1749	1767	0.75	0.837
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1754	1772	0.75	0.815
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	1757	1773	0.89	0.848
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1761	1771	0.75	0.815
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	1777	1793	1	0.996
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF3.01	0.99	1778	1794	1	0.995
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1780	1794	1	0.923
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1787	1803	1	0.967
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1790	1806	1	0.972



TABLE 9-continued

Boxes and Motifs identified in the starting sequence of the p-GOS2 promoter							
p-GOS2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	Position	Position	sim.	sim.
				from-to	—	—	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1803	1819	0.75	0.797
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1847	1863	1	0.945
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1850	1866	1	0.966
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	1866	1886	1	0.916
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1872	1888	1	0.905
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	1873	1889	1	0.837
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1878	1888	1	0.902
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1882	1898	0.75	0.824
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1886	1896	0.97	0.949
P\$EPFF	EPF-type zinc finger factors, two canonical Cys2/His2 zinc finger motifs separated by spacers of various length	P\$ZPT22.01	0.75	1887	1909	1	0.774
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	1907	1921	1	0.903
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1912	1930	1	0.849
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	1920	1934	1	0.892
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	1927	1937	1	0.984
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	1973	1989	1	0.9
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1998	2014	1	0.971
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	2001	2017	1	0.83
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	2018	2034	1	0.964
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	2021	2037	1	0.957
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	2035	2045	1	0.858
P\$MIIG	MYB IIG-type binding sites	P\$MYBC1.01	0.92	2033	2047	1	0.941
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	2041	2057	1	0.792
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	2054	2070	1	0.918
P\$GTBX	GT-box elements	P\$GT1.01	0.85	2056	2072	1	0.876
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	2067	2075	1	0.906
P\$EINL	Ethylene insensitive 3 like factors	P\$TEIL.01	0.92	2098	2106	0.96	0.926
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	2110	2126	1	0.828
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	2110	2126	1	0.807

TABLE 10

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	Position	Position	sim.	sim.
				from-to	—	—	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	6	16	1	0.857
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	15	29	1	0.832
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	29	45	1	0.92
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	33	49	1	0.897
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	35	55	0.79	0.82
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$IDEF2.01	0.96	48	60	1	0.96
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	48	64	1	0.954
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	60	74	1	0.887
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	61	77	1	0.961

TABLE 10-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	65 75	0.97	0.94	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	69 85	1	0.867	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	71 87	0.89	0.92	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	74 90	1	0.832	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	75 91	1	0.877	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	76 92	0.75	0.781	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	77 93	0.76	0.835	
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXL.01	0.8	118 132	0.77	0.841	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	126 142	1	0.99	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	149 165	1	0.989	
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	170 192	0.81	0.712	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	187 203	1	0.878	
P\$E2FF	E2F-homolog cell cycle regulators	P\$E2F.01	0.82	193 207	1	0.826	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	207 217	0.83	0.903	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	207 217	1	0.967	
P\$CNAC	Calcium regulated NAC-factors	P\$CBNAC.02	0.85	215 235	1	0.937	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	217 233	1	0.944	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	216 236	1	0.735	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	222 238	1	0.979	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	246 262	1	0.901	
P\$STKM	Storekeeper motif	P\$STK.01	0.85	251 265	1	0.85	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	254 264	0.83	0.904	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	254 264	1	0.998	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	284 300	1	0.757	
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	297 311	1	0.94	
P\$LFYB	LFY binding site	P\$LFY.01	0.93	318 330	0.91	0.945	
P\$WBXF	W Box family	P\$ERE.01	0.89	322 338	1	0.893	
P\$GAGA	GAGA elements	P\$BPC.01	1	329 353	1	1	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	335 349	0.75	0.865	
P\$GAGA	GAGA elements	P\$BPC.01	1	331 355	1	1	
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	337 351	1	0.968	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	341 357	1	0.875	
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	345 365	1	0.925	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	363 377	1	0.924	
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	383 399	1	0.895	
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	388 406	1	0.8	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	397 407	1	0.902	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	395 411	1	0.889	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	396 412	1	0.844	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	398 412	1	0.892	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	397 413	0.75	0.781	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	400 410	1	0.902	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	402 418	0.75	0.781	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	405 421	1	0.983	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	408 422	1	0.917	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene	P\$OCSTF.01	0.73	426 446	1	0.762	

TABLE 10-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
	(OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA						
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	440 450	1	0.926	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	444 454	1	1	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	447 463	1	0.819	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	472 482	1	0.988	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	481 497	1	0.922	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	482 498	1	0.994	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	482 498	1	0.9	
P\$WBXF	W Box family	P\$WRKY11.01	0.94	493 509	1	0.957	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	504 514	1	0.988	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	509 525	1	0.961	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	515 525	1	0.948	
P\$GTBX	GT-box elements	P\$SIF.01	0.79	518 534	0.75	0.793	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	527 537	1	0.897	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	525 541	0.75	0.78	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	539 555	0.75	0.782	
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	568 592	0.75	0.772	
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	591 607	1	0.837	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	599 607	1	0.867	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	629 645	1	0.888	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	631 647	0.75	0.831	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	631 647	0.8	0.783	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	638 654	1	0.861	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	649 663	1	0.899	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	687 703	1	0.987	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	689 705	1	0.888	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	695 705	1	0.929	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	694 708	1	0.954	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	701 711	1	0.98	
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	711 725	1	0.929	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.9	716 726	0.79	0.901	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	716 726	1	0.998	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	716 732	1	0.893	
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	715 733	1	0.856	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	718 734	0.76	0.762	
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	718 734	1	0.833	
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	733 747	1	0.917	
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	744 760	0.78	0.834	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	754 770	0.75	0.831	
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	756 770	0.75	0.869	
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$OSBHLH66.01	0.85	789 807	1	0.851	
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	793 809	1	0.998	
P\$URNA	Upstream sequence element of U-snRNA genes	P\$USE.01	0.75	812 828	0.75	0.797	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	812 832	1	0.895	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	813 833	0.92	0.911	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	872 882	0.81	0.888	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	879 889	1	0.896	

TABLE 10-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	880 894	1	0.877	
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	900 916	0.95	0.968	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	909 925	1	0.905	
P\$MYBL	MYB-like proteins	P\$AS1_AS2_I.01	0.99	911 927	1	1	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	981 991	1	0.893	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	982 996	1	0.951	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	982 998	1	0.884	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	983 999	1	0.955	
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	1006 1026	0.83	0.8	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1008 1024	0.78	0.811	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1010 1024	1	0.91	
P\$CGCG	Calmodulin binding/CGCG box binding proteins	P\$ATSR1.01	0.84	1051 1067	1	0.859	
P\$ABRE	ABA response elements	P\$ABF1.01	0.79	1053 1069	1	0.837	
P\$CE3S	Coupling element 3 sequence	P\$CE3.01	0.77	1052 1070	1	0.863	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC092.01	0.92	1055 1067	1	0.927	
P\$DPBF	Dc3 promoter binding factors	P\$DPBF.01	0.89	1057 1067	1	0.908	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1059 1089	1	0.806	
O\$MTEN	Core promoter motif ten elements	O\$HMTE.01	0.88	1072 1092	0.96	0.94	
P\$DREB	Dehydration responsive element binding factors	P\$HVDRF1.01	0.89	1079 1093	1	0.917	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1077 1107	1	0.807	
O\$MTEN	Core promoter motif ten elements	O\$DMTE.01	0.77	1097 1117	0.84	0.805	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.02	0.87	1135 1151	1	0.915	
P\$SALT	Salt/drought responsive elements	P\$ALFIN1.02	0.95	1136 1150	1	0.954	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	1179 1195	1	0.882	
P\$SBPD	SBP-domain proteins	P\$SBP.01	0.88	1199 1215	1	0.912	
P\$PALA	Conserved box A in PAL and 4CL gene promoters	P\$PALBOXA.01	0.84	1201 1219	1	0.863	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1230 1246	1	0.833	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1244 1254	1	0.89	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1244 1254	0.75	0.777	
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	1248 1268	0.97	0.835	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1262 1278	1	0.953	
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	1278 1294	1	0.864	
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1277 1303	1	0.871	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$OSMYBS.01	0.82	1343 1359	0.75	0.822	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1349 1359	0.97	0.955	
P\$STKM	Storekeeper motif	P\$STK.01	0.85	1355 1369	1	0.927	
P\$GTBX	GT-box elements	P\$GT1.01	0.85	1403 1419	0.97	0.865	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1437 1457	0.77	0.703	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1478 1494	1	0.764	
P\$WBXF	W Box family	P\$ERE.01	0.89	1488 1504	1	0.968	
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1491 1511	0.96	0.852	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$HVMCB1.01	0.93	1498 1514	1	0.934	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	1509 1525	0.75	0.837	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	1551 1565	1	0.82	

TABLE 10-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to		sim.	sim.
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	1558 1574		1	0.883
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569 1579		0.83	0.904
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569 1579		0.94	0.978
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1609 1625		0.75	0.781
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	1613 1623		1	0.966
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1617 1637		0.84	0.761
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	1625 1647		0.9	0.75
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC019.01	0.94	1632 1644		0.95	0.968
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1642 1658		1	0.882
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	1644 1660		1	0.864
P\$MYBL	MYB-like proteins	P\$MYBPH3.01	0.8	1647 1663		1	0.938
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	1694 1710		1	1
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1703 1719		0.86	0.765
P\$CCAF	Circadian control factors	P\$EE.01	0.84	1719 1733		1	0.955
P\$MADS	MADS box proteins	P\$AG.01	0.8	1717 1737		0.9	0.816
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1732 1748		1	0.98
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1749 1759		1	0.957
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1749 1767		0.75	0.837
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1754 1772		0.75	0.815
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	1757 1773		0.89	0.848
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1761 1771		0.75	0.815
P\$MADS	MADS box proteins	P\$AGL3.01	0.83	1768 1788		0.97	0.838
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	1777 1793		1	0.996
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF3.01	0.99	1778 1794		1	0.995
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1780 1794		1	0.923
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1787 1803		1	0.967
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1790 1806		1	0.972
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1803 1819		0.75	0.797
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1847 1863		1	0.945
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1850 1866		1	0.966
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	1866 1886		1	0.916
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1872 1888		1	0.905
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	1873 1889		1	0.837
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1878 1888		1	0.902
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1882 1898		0.75	0.824
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1886 1896		0.97	0.949
P\$EPFF	EPF-type zinc finger factors, two canonical Cys2/His2 zinc finger motifs separated by spacers of various length	P\$ZPT22.01	0.75	1887 1909		1	0.752
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	1907 1921		1	0.903
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1912 1930		1	0.849
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	1920 1934		1	0.892
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	1927 1937		1	0.984
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	1973 1989		1	0.9
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1998 2014		1	0.958
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	2001 2017		1	0.875
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	2018 2034		1	0.964
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	2021 2037		1	0.957

TABLE 10-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm1 promoter.							
p-GOS2_perm1				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	2035 2045	1	0.868	
P\$MIIG	MYB IIG-type binding sites	P\$MYBC1.01	0.92	2033 2047	1	0.938	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	2041 2057	1	0.792	
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	2054 2070	1	0.918	
P\$GTBX	GT-box elements	P\$GT1.01	0.85	2056 2072	1	0.876	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	2067 2075	1	0.906	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	2075 2083	1	0.906	
P\$EINL	Ethylene insensitive 3 like factors	P\$TEIL.01	0.92	2098 2106	0.96	0.926	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	2110 2126	1	0.828	
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	2110 2126	1	0.807	

TABLE 11

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	6 16	1	0.857	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	15 29	1	0.832	
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	29 45	1	0.95	
P\$MYBL	MYB-like proteins	P\$WER.01	0.87	33 49	1	0.897	
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	35 55	0.789	0.82	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$IDF2.01	0.96	48 60	1	0.96	
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	48 64	1	0.954	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	60 74	1	0.883	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	61 77	1	0.961	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	65 75	0.969	0.94	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	69 85	1	0.867	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	71 87	0.892	0.92	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	74 90	1	0.832	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	75 91	1	0.877	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	76 92	0.75	0.781	
O\$YTBP	Yeast TATA binding protein factor	O\$SPT15.01	0.83	77 93	0.755	0.835	
P\$MIIG	MYB IIG-type binding sites	P\$PALBOXL.01	0.8	118 132	0.768	0.841	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	126 142	1	0.99	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	149 165	1	0.989	
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	170 192	0.812	0.713	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	187 203	1	0.869	
P\$E2FF	E2F-homolog cell cycle regulators	P\$E2F.01	0.82	193 207	1	0.829	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	200 210	0.969	0.945	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	207 217	0.83	0.903	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	207 217	1	0.967	

TABLE 11-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$CNAC	Calcium regulated NAC-factors	P\$CBNAC.02	0.85	215 235	1	0.95	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	217 233	1	0.975	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	216 236	1	0.71	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$PHR1.01	0.84	222 238	1	0.922	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	246 262	1	0.901	
P\$STKM	Storekeeper motif	P\$STK.01	0.85	251 265	1	0.85	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	254 264	0.83	0.904	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	254 264	1	0.998	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	284 300	1	0.784	
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	297 311	1	0.947	
P\$LFYB	LFY binding site	P\$LFY.01	0.93	318 330	0.914	0.945	
P\$GAGA	GAGA elements	P\$BPC.01	1	329 353	1	1	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	335 349	0.75	0.865	
P\$GAGA	GAGA elements	P\$BPC.01	1	331 355	1	1	
P\$CCAF	Circadian control factors	P\$CCA1.01	0.85	337 351	1	0.968	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	341 357	1	0.875	
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	345 365	1	0.925	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	363 377	1	0.925	
O\$VTBP	Vertebrate TATA binding protein factor	O\$MTATA.01	0.84	383 399	1	0.91	
P\$CARM	CA-rich motif	P\$CARICH.01	0.78	388 406	1	0.785	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	397 407	1	0.902	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	395 411	1	0.889	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	396 412	1	0.844	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.01	0.88	398 412	1	0.892	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	397 413	0.75	0.781	
P\$NCS2	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	400 410	1	0.902	
P\$MSAE	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	402 418	0.75	0.781	
P\$MYBL	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	405 421	1	0.983	
P\$MYBL	Plant TATA binding protein factor	O\$PTATA.02	0.9	408 422	1	0.917	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSTF.01	0.73	426 446	1	0.733	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	440 450	1	0.921	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$WUS.01	0.94	444 454	1	1	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GCN4.01	0.81	447 463	1	0.819	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	472 482	1	0.987	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	481 497	1	0.922	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	482 498	1	0.994	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	482 498	1	0.9	
P\$WBXF	W Box family	P\$WRKY11.01	0.94	493 509	1	0.957	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	504 514	1	0.998	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	509 525	1	0.986	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	515 525	1	0.948	
P\$GTBX	GT-box elements	P\$S1F.01	0.79	518 534	0.75	0.793	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	527 537	1	0.897	

TABLE 11-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position		Core	Matrix
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	525 541	0.75	0.825	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	539 555	0.75	0.782	
P\$ROOT	Root hair-specific cis-elements in angiosperms	P\$RHE.01	0.77	568 592	0.75	0.787	
P\$ABRE	ABA response elements	P\$ABRE.01	0.82	591 607	1	0.837	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	599 607	1	0.867	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	629 645	1	0.883	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$HDG9.01	0.77	631 647	0.797	0.776	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	638 654	1	0.886	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	649 663	1	0.891	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBF.01	0.97	687 703	1	0.987	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	689 705	1	0.888	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	695 705	1	0.929	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	694 708	1	0.954	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	701 711	1	1	
P\$MADS	MADS box proteins	P\$RIN.01	0.77	699 719	1	0.776	
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	711 725	1	0.924	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB1.01	0.9	716 726	0.789	0.901	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$BLR.01	0.9	716 726	1	0.998	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	716 732	1	0.893	
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	715 733	1	0.856	
P\$DOFF	DNA binding with one finger (DOF)	P\$PBOX.01	0.75	718 734	0.761	0.762	
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	718 734	1	0.833	
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	733 747	1	0.885	
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	744 760	0.779	0.834	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	754 770	0.75	0.831	
P\$TELO	Telo box (plant interstitial telomere motifs)	P\$ATPURA.01	0.85	756 770	0.75	0.869	
P\$MYCL	Myc-like basic helix-loop-helix binding factors	P\$OSBHLH66.01	0.85	789 807	1	0.851	
P\$BRRE	Brassinosteroid (BR) response element	P\$BZR1.01	0.95	793 809	1	0.998	
P\$URNA	Upstream sequence element of U-snRNA genes	P\$USE.01	0.75	812 828	0.75	0.797	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	812 832	1	0.895	
P\$MADS	MADS box proteins	P\$AGL1.01	0.84	813 833	0.915	0.911	
P\$NCS1	Nodulin consensus sequence 1	P\$NCS1.01	0.85	872 882	0.805	0.888	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	879 889	1	0.896	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	880 894	1	0.877	
P\$MYBL	MYB-like proteins	P\$NTMYBAS1.01	0.96	900 916	0.949	0.968	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	909 925	1	0.905	
P\$MYBL	MYB-like proteins	P\$AS1_AS2_I.01	0.99	911 927	1	1	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	981 991	1	0.893	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	982 996	1	1	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	982 998	1	0.884	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.01	0.9	983 999	1	0.973	
P\$MADS	MADS box proteins	P\$AGL15.01	0.79	1006 1026	0.825	0.793	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1008 1024	0.778	0.811	



TABLE 11-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1010 1024	1	0.91	
P\$CGCG	Calmodulin binding/CGCG box binding proteins	P\$ATSR1.01	0.84	1051 1067	1	0.859	
P\$ABRE	ABA response elements	P\$ABF1.01	0.79	1053 1069	1	0.797	
P\$CE3S	Coupling element 3 sequence	P\$CE3.01	0.77	1052 1070	1	0.874	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC092.01	0.92	1055 1067	1	0.924	
P\$DPBF	Dc3 promoter binding factors	P\$DPBF.01	0.89	1057 1067	1	0.908	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1059 1089	1	0.806	
O\$MTEN	Core promoter motif ten elements	O\$HMTE.01	0.88	1072 1092	0.961	0.94	
P\$DREB	Dehydration responsive element binding factors	P\$HVDRF1.01	0.89	1079 1093	1	0.922	
P\$PREM	Motifs of plastid response elements	P\$MGPROTORE.01	0.77	1077 1107	1	0.784	
O\$MTEN	Core promoter motif ten elements	O\$DMTE.01	0.77	1097 1117	0.844	0.802	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.02	0.87	1135 1151	1	0.915	
P\$SALT	Salt/drought responsive elements	P\$ALFIN1.02	0.95	1136 1150	1	0.954	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$PDF2.01	0.85	1179 1195	1	0.882	
P\$SBPD	SBP-domain proteins	P\$SBP.01	0.88	1199 1215	1	0.912	
P\$PALA	Conserved box A in PAL and 4CL gene promoters	P\$PALBOXA.01	0.84	1201 1219	1	0.863	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$ZMMRP1.01	0.79	1230 1246	1	0.838	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1244 1254	1	0.777	
P\$MADS	MADS box proteins	P\$AGL2.01	0.82	1248 1268	0.969	0.828	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1262 1278	1	0.953	
P\$HEAT	Heat shock factors	P\$HSE.01	0.81	1278 1294	1	0.864	
P\$LEGB	Legumin Box family	P\$RY.01	0.87	1277 1303	1	0.871	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$OSMYBS.01	0.82	1343 1359	0.75	0.822	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1349 1359	0.969	0.955	
P\$STKM	Storekeeper motif	P\$STK.01	0.85	1355 1369	1	0.95	
P\$GTBX	GT-box elements	P\$GT1.01	0.85	1403 1419	0.969	0.85	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1439 1455	0.75	0.797	
P\$OCSE	Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA	P\$OCSL.01	0.69	1437 1457	0.769	0.734	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1478 1494	1	0.764	
P\$WBXF	W Box family	P\$WRKY.01	0.92	1488 1504	1	0.94	
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1491 1511	0.957	0.859	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$HVMCB1.01	0.93	1498 1514	1	0.934	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$TAMYB80.01	0.83	1509 1525	0.75	0.845	
P\$MSAE	M-phase-specific activator elements	P\$MSA.01	0.8	1551 1565	1	0.807	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2.01	0.87	1558 1574	1	0.883	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569 1579	0.83	0.904	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB5.01	0.89	1569 1579	0.936	0.978	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1609 1625	0.75	0.781	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	1613 1623	1	0.966	

TABLE 11-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position			
Family	Further Family Information	Matrix	Opt.	from-to	Core	Matrix	
					sim.	sim.	
P\$TEFB	TEF-box	P\$TEF1.01	0.76	1617 1637	0.839	0.812	
P\$WNAC	Wheat NAC-domain transcription factors	P\$TANAC69.01	0.68	1625 1647	0.896	0.811	
P\$NACF	Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors	P\$ANAC019.01	0.94	1632 1644	0.953	0.968	
P\$GTBX	GT-box elements	P\$S1F.01	0.79	1642 1658	1	0.917	
P\$PSRE	Pollen-specific regulatory elements	P\$GAAA.01	0.83	1644 1660	1	0.864	
P\$MYBL	MYB-like proteins	P\$MYBPH3.01	0.8	1647 1663	1	0.938	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF1.01	0.98	1694 1710	1	1	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	1703 1719	0.857	0.757	
P\$CCAF	Circadian control factors	P\$EE.01	0.84	1719 1733	1	0.953	
P\$MADS	MADS box proteins	P\$AG.01	0.8	1717 1737	0.902	0.813	
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1732 1748	1	0.967	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1749 1759	1	0.965	
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1749 1767	0.75	0.83	
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1754 1772	0.75	0.822	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.02	0.76	1757 1773	0.89	0.848	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$ATHB9.01	0.77	1761 1771	0.75	0.815	
O\$VTBP	Vertebrate TATA binding protein factor	O\$VTATA.02	0.89	1777 1793	1	0.996	
P\$DOFF	DNA binding with one finger (DOF)	P\$DOF3.01	0.99	1778 1794	1	0.995	
O\$PTBP	Plant TATA binding protein factor	O\$PTATA.02	0.9	1780 1794	1	0.923	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1787 1803	1	0.967	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1790 1806	1	0.972	
O\$VTBP	Vertebrate TATA binding protein factor	O\$ATATA.01	0.78	1803 1819	0.75	0.812	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	1847 1863	1	0.945	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	1850 1866	1	0.966	
P\$MADS	MADS box proteins	P\$SQUA.01	0.9	1866 1886	1	0.916	
P\$GTBX	GT-box elements	P\$SBF1.01	0.87	1872 1888	1	0.905	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	1873 1889	1	0.837	
P\$AHBP	<i>Arabidopsis</i> homeobox protein	P\$HAHB4.01	0.87	1878 1888	1	0.902	
P\$L1BX	L1 box, motif for L1 layer-specific expression	P\$ATML1.01	0.82	1882 1898	0.75	0.824	
O\$INRE	Core promoter initiator elements	O\$DINR.01	0.94	1886 1896	0.969	0.949	
P\$EPFF	EPF-type zinc finger factors, two canonical Cys2/His2 zinc finger motifs separated by spacers of various length	P\$ZPT22.01	0.75	1887 1909	1	0.755	
P\$GAPB	GAP-Box (light response elements)	P\$GAP.01	0.88	1907 1921	1	0.903	
P\$SUCB	Sucrose box	P\$SUCROSE.01	0.81	1912 1930	1	0.849	
P\$HMGF	High mobility group factors	P\$HMG_IY.01	0.89	1920 1934	1	0.892	
P\$SEF4	Soybean embryo factor 4	P\$SEF4.01	0.98	1927 1937	1	0.984	
P\$MYBL	MYB-like proteins	P\$ATMYB77.01	0.87	1973 1989	1	0.894	
P\$GTBX	GT-box elements	P\$ASIL1.01	0.93	1998 2014	1	0.971	
P\$OPAQ	Opaque-2 like transcriptional activators	P\$O2_GC4.01	0.81	2001 2017	1	0.83	
P\$IBOX	Plant I-Box sites	P\$GATA.01	0.93	2018 2034	1	0.964	
P\$MYBS	MYB proteins with single DNA binding repeat	P\$MYBST1.01	0.9	2021 2037	1	0.957	
P\$LREM	Light responsive element motif, not modulated by different light qualities	P\$RAP22.01	0.85	2035 2045	1	0.858	
P\$MIIG	MYB IIG-type binding sites	P\$MYBC1.01	0.92	2033 2047	1	0.941	
P\$HEAT	Heat shock factors	P\$HSFA1A.01	0.75	2041 2057	1	0.801	
P\$MYBL	MYB-like proteins	P\$GAMYB.01	0.91	2054 2070	1	0.918	

TABLE 11-continued

Boxes and Motifs identified in the permuted sequence of the p-GOS2_perm2 promoter.							
p-GOS2_perm2				Position	Core	Matrix	
Family	Further Family Information	Matrix	Opt.	from-to	sim.	sim.	
P\$GTBX	GT-box elements	P\$GT1.01	0.85	2056 2072	1	0.876	
P\$ASRC	AS1/AS2 repressor complex	P\$AS1_AS2_II.01	0.86	2067 2075	1	0.906	
P\$EINL	Ethylen insensitive 3 like factors	P\$TEIL.01	0.92	2098 2106	0.964	0.926	
O\$VTBP	Vertebrate TATA binding protein factor	O\$LTATA.01	0.82	2110 2126	1	0.828	
P\$MYBL	MYB-like proteins	P\$MYBPH3.02	0.76	2110 2126	1	0.807	

15

### 5.2 Vector Construction

The DNA fragments representing promoter p-GOS2\_perm1 (SEQ ID NO14) and p-GOS2\_perm2 (SEQ ID NO15), respectively, were generated by gene synthesis. Endonucleolytic restriction sites suitable for cloning the promoter fragments were included in the synthesis.

The p-GOS2\_perm1 (SEQ ID NO14) and p-GOS2\_perm2 (SEQ ID NO15) promoters are cloned into destination vectors compatible with the Multisite Gateway System upstream of an attachment site and a terminator using *Sma*I restriction endonuclease.

beta-Glucuronidase (GUS) or *uidA* gene which encodes an enzyme for which various chromogenic substrates are known, is utilized as reporter protein for determining the expression features of the permuted p-GOS2\_perm (SEQ ID NO14) and p-GOS2\_perm2 (SEQ ID NO15) promoter sequences.

A pENTR/A vector harboring the beta-Glucuronidase reporter gene *c-GUS* (with the prefix *c-* denoting coding sequence) is constructed using site specific recombination (BP-reaction).

By performing a site specific recombination (LR-reaction), the created pENTR/A is combined with the destination vector according to the manufacturers (Invitrogen, Carlsbad, Calif., USA) Multisite Gateway manual. The reaction yields a binary vector with the p-GOS2\_perm1 promoter (SEQ ID NO14) or the p-Gos2\_perm2 promoter (SEQ ID NO 15), respectively, the beta-Glucuronidase coding sequence *c-GUS* and a terminator.

### 5.3 Generation do Transgenic Rice Plants

The *Agrobacterium* containing the respective expression vector is used to transform *Oryza sativa* plants. Mature dry seeds of the rice *japonica* cultivar Nipponbare are dehusked. Sterilization is carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2% HgCl<sub>2</sub>, followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds are then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli are excised and propagated on the same medium. After two weeks, the calli are multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces are sub-cultured on fresh medium 3 days before co-cultivation (to boost cell division activity).

*Agrobacterium* strain LBA4404 containing the respective expression vector is used for co-cultivation. *Agrobacterium* is inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28° C. The bacteria are then collected and suspended in liquid co-cultivation medium to a density (OD<sub>600</sub>) of about 1. The suspension is then

transferred to a Petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues are then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25° C. Co-cultivated calli are grown on 2,4-D-containing medium for 4 weeks in the dark at 28° C. in the presence of a selection agent During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential is released and shoots developed in the next four to five weeks. Shoots are excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they are transferred to soil. Hardened shoots are grown under high humidity and short days in a greenhouse.

The primary transformants are transferred from a tissue culture chamber to a greenhouse. After a quantitative PCR analysis to verify copy number of the T-DNA insert, only single copy transgenic plants that exhibit tolerance to the selection agent are kept for harvest of T1 seed. Seeds are then harvested three to five months after transplanting. The method yields single locus transformants at a rate of over 50% (Aldemita and Hodges 1996, Chan et al. 1993, Hiei et al. 1994).

#### Example 6: Expression Profile of the p-GOS2\_perm1 (SEQ ID NO14) and p-GOS2\_perm2 (SEQ ID NO15) Control Elements

To demonstrate and analyze the transcription regulating properties of a promoter, it is useful to operably link the promoter or its fragments to a reporter gene, which can be employed to monitor its expression both qualitatively and quantitatively. Preferably bacterial  $\beta$ -glucuronidase is used (Jefferson 1987).  $\beta$ -glucuronidase activity can be monitored in planta with chromogenic substrates such as 5-bromo-4-Chloro-3-indolyl- $\beta$ -D-glucuronic acid during corresponding activity assays (Jefferson 1987). For determination of promoter activity and tissue specificity, plant tissue is dissected, stained and analyzed as described (e.g., Bäumlein 1991).

The regenerated transgenic T0 rice plants are used for reporter gene analysis.

General results for SEQ ID NO14: Medium-strong GUS expression is detected in all plant tissues analyzed.

General results for SEQ ID NO15: Medium-strong GUS expression is detected in all plant tissues analyzed.

General results for SEQ ID NO13: Medium-strong GUS expression is detected in all plant tissues analyzed.

## SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 15

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 <212> TYPE: DNA  
 <213> ORGANISM: Phaseolus vulgaris  
 <220> FEATURE:  
 <221> NAME/KEY: Promoter  
 <222> LOCATION: (1)..(1151)  
 <223> OTHER INFORMATION: p-PvArc

<400> SEQUENCE: 1

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cttatctctt tgtttctgta ataataatat aagagactta aacttttaat ataataattg     180
taattagggt ttctagtcac gagcaccact cagagacaag atttcaagaa aacaattttg     240
ttaaacatct tattagaaac ttttagttaa gtcttgaagt tagaattaa caaaaaaag       300
tacacacgag aacacaata aaccactac cgtcagggta tcataaggat gaaatgtttt       360
gatatcatta aatataacac acacaaaaat acatctaatt ataacaatat atgttatata      420
tatatttttg taaaaactta gagtttttca aaacattcta atacatgatt agagtttata      480
gaaatacaaa tatttaaaaa atataatfff aaaaaaacat tctaaagtca ttcagatcct     540
ctcacacctg tgtgatcatt tagtcatgta tgtagtaca tcattgtagt tcacaacaga      600
gtaaaataaa taaggataaa ctagggaata tatataatat atacaattaa ataaaaaagg     660
gaaaatcaaa ttagaatttt agattcccca catgacacaa ctcacatgc acgctgccac      720
ctcagctccc tcctctccac acatgtctca tgctactttc gactttggtt ttttactat      780
gacacaactc gccatgcatg ttgccacgtg agctccttcc tcttcccatg atgacaccac     840
tgggcatgca tgctgccacc tcagctccca cctcttctca ttatgagcct actggccatg     900
cacactgcca cctcagcact cctctcactt cccattgcta cctgccaac cgcttctctc     960
cataaatatc tatttaaat taaactaatt atttcatata cttttttgat gacgtggatg    1020
cattgccatc gttgtttaat aattgttaat ttggagttga ataataaaat gaaagaaaaa    1080
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tgaatgcatg a                                     1151

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 <223> OTHER INFORMATION: Promoter  
 <220> FEATURE:  
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 <222> LOCATION: (1)..(1151)  
 <223> OTHER INFORMATION: p-PvArc-perm

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cttatctctt tgtttctgta ataataatat aagtgtgata aacttttaat ataataattg     180
taattagggt ttctacagat gagcaccact cagagacaag ataagaagaa aacaattttg     240
ttaaacatga ttatagaaac ttttagttaa gtcttgaagt atcaatataa caaaaaaag      300
tacacacgac tatgacaata aaccactac cgtcagggta tcatttcgat gaaatgtttt     360

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gaaatacaat taaataaaaa atataatfff aaaaaaacat agtaaagtca atgagatcct 540
ctctgacctc agtgatcatt tagtcatgta tgtacaacaa tcattgttca tcacatgact 600
gtaaaataaa taaggataaa cttgggaata tatataatat attgtattaa ataaaaaagg 660
gaaatacaaa tatcaatfff agattcccga gttgacacaa ctcacatgc acgctgccac 720
ctcagctccc agctctcgtc acatgtctca tgtcagttag gtctttggtt tttagtcttt 780
gacacaactc gccatgcatg ttgccacgtg agctcgttcc tcttcccag atctcaccac 840
tgggcatgca tgctgccacc tcagctggca cctcttctct atatgtccct agaggccatg 900
cacagtgcca cctcagcact cctctcagaa cccatacgtc cctgccaatc ggcttctctc 960
cataaatatc tatttaaatt ataactaatt atttcatata ctttaattgat gacgtggatg 1020
cattgccatc gttgtttaat aattgttaat tacgacatga taaataaaat gaaagtaaaa 1080
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tgaatgcatg a 1151

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<210> SEQ ID NO 3
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<212> TYPE: DNA
<213> ORGANISM: Vicia faba
<220> FEATURE:
<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(1799)
<223> OTHER INFORMATION: p-VfSBP

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<400> SEQUENCE: 3

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actcttgcaa actctgattg aacctacgtg aaaactgctc cagaagttct aaccaaattc 180
cgtcttggga aggcccaaaa tttattgagt acttcagttt catggacgtg tcttcaaaga 240
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aatcatcaca ttataattat tgccttatt taaaattatg ataaagttgt atcattaaga 1020
ttgagaaaac caaatagtcc tegtcttgat ttttgaatta ttgttttcta tgttactttt 1080
cttcaagcct atataaaaa tttgtaatgc taaattgtat gctggaaaaa aatgtgtaat 1140

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aaccttggtg gaatgttaaa ggtaataaaa cattcagaat tatgaccatc tattaatata 1560
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gctggcctgt gtatatcaat tccatttcca gatggtagaa actgccacta cgaataatta 1680
gtcataagac acgtatgta acacacgtcc ccttgcattg tttttgcat atattccgtc 1740
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(1799)
<223> OTHER INFORMATION: p-VfSBP-perm

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<400> SEQUENCE: 4

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actcttgcaa tgactgattg aacctacgtg aaaactgctg gtcaagttct aaccaaattc 180
cgtctacgga aggcccaaaa tttattgaca tcttcagttt catggacgtg tcttcaaagt 240
tttataactt cttatcccat catttttaag tctagttctg ttccgcatag tcttagatct 300
caaacaaatc tacaactctt gtgtcagttc ttcttccaga atcaacttgc tacatggtga 360
aaatctggcg tcaagttctg aacttgtaa ttttcttaac agttagaaaa taatctaagt 420
gtttagaata ttgacttttc caaagcaaag aagacttttg actttcttaa taaaacaaac 480
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tcaaagtttg acttttcaga ctgcaattga ccattttgca gaagtgccaa ttccaaacca 600
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gttacctttg tgcagaactt aagagcaact tacagactca tttactaaaa tactacaatc 840
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<211> LENGTH: 1138
<212> TYPE: DNA
<213> ORGANISM: Vicia faba
<220> FEATURE:
<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(1138)
<223> OTHER INFORMATION: p-VfNapin

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acattttaa tttcactatt ggctgaatgc ttcttctttg aggaagaaac aattcagatg 180
gcagaaatgt atcaaccaat gcatatatac aaatgtacct cttgttctca aaacatctat 240
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ttattactat tttcatgcca gggtgacctg tacattatat ttgtaaggat tgacgctatt 360
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: p-VfNapin-perm

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atcaaggact attggttatt agtctgtccg ttatttgaat atgataacgc aaggtttccg    180
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&lt;210&gt; SEQ ID NO 7

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Transformation Vector

&lt;400&gt; SEQUENCE: 7

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gcgatcaccg cttccccat gatgtttaac tttgttttag ggcgactgcc ctgctgcgta 15420
acatcgttgc tgctcataa catcaaacat cgaccacgg cgtaacgcgc ttgctgcttg 15480
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actgcgttcc at 15552

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<210> SEQ ID NO 11
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 11

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34

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<210> SEQ ID NO 12  
 <211> LENGTH: 37  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 12

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<210> SEQ ID NO 13  
 <211> LENGTH: 2194  
 <212> TYPE: DNA  
 <213> ORGANISM: *Oryza sativa*  
 <220> FEATURE:  
 <221> NAME/KEY: Promoter  
 <222> LOCATION: (1)..(2194)  
 <223> OTHER INFORMATION: p-GOS2

<400> SEQUENCE: 13

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 aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120  
 catccaccta ctttagtggc aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180  
 tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240  
 tctgtcatga agttaaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata 300  
 aaaaaatctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360  
 atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420  
 ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480  
 tttagtaatta aagacaattg acttattttt attatttattc ttttttcgat tagatgcaag 540  
 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600  
 tcaactagca acacatctct aatatcactc gcctatttta tacatttagg tagcaatattc 660  
 tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa tacaanaaat 720  
 aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780  
 aaaaaagaa ttttgctcgt gcgagagcgc caatctccca tattgggcac acaggcaaca 840  
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 tccgcaacaa ccttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa 960  
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ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatatac ttaaaaagtc 1740
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atctctgata tccattttta attatatgaa atgaactgta gcataagcag tattcatttg 1920
gattatTTTT tttattagct ctcacccctt cattattctg agctgaaagt ctggcatgaa 1980
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<210> SEQ ID NO 14
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<220> FEATURE:
<223> OTHER INFORMATION: Promoter
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<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(2194)
<223> OTHER INFORMATION: p-GOS2_perm1

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<400> SEQUENCE: 14

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atggagatat tctgaacgta ttggcaaagt tttaaacata taattatata attttatagg 420
ttgtgcatcc gtcatttgc acatcattaa ggacatgtct tactccatcc cgatttttat 480
ttagtaatta aagacaattg acttcttttt attatttatac ttttttcgat tagatgcagg 540
gtacttacgc acacactttg tgctcatgtg catctgtgag tgcacctcct caatacacgt 600
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tgaattcaag cactcgacca tcaccagacc acttttaata atatctaaac tacaaaaaat 720
aattttacag aatagcatga aaaatatgaa acgaactatt taggtttttc acatacacia 780
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ctaataaagt acggttggtt ggccctcgat tctggttggt atgcttctcg atttgaccag 1500
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gatgagattg aatgattgaa tcttaagcct gtccaaaact tcgcagctgg cttgtttaga 1620
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<210> SEQ ID NO 15
<211> LENGTH: 2194
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Promoter
<220> FEATURE:
<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(2194)
<223> OTHER INFORMATION: p-GOS2_perm2

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<400> SEQUENCE: 15

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catccaccta ctttagtggc aataaggcta aataaaaaag agtcgctaca ccagtttctg 180
tttcttagt aattaagggg gaaaatgaaa tcattattgc ttagcatata cgttcacagc 240
tctgtcatga agttaaatta ttcgaggtag ccttaattgt catcaaactc ttcttgaatc 300
aaaaaatctt tctagctgaa ctcaatgggt acagagagag atttttttta aaaaaataga 360
atcaagatat tctgaacgta ttggcagaga tttaaacata taattatata attttatagt 420
tcgtgcattc gtcatatcgc agatcattaa ggacatgtct tactccatcc cagtttttat 480
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ttggtgtagc	ttgtcacttt	caccagcaaa	gttc			2194

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The invention claimed is:

1. A synthetic promoter comprising SEQ ID NO: 4.
2. An expression construct comprising the synthetic promoter of claim 1 operably linked to a nucleotide sequence of interest.
3. A vector comprising the expression construct of claim 2.
4. A host cell comprising the synthetic promoter of claim 1.
5. The host cell of claim 4, wherein said host cell is a plant cell.
6. A plant or plant part comprising the synthetic promoter of claim 1.

7. A plant seed comprising the synthetic promoter of claim 1.

8. A method of making a transgenic plant or plant cell, the method comprising:

- a) transforming a plant or plant cell with a construct comprising SEQ ID NO: 4 operably linked to a sequence of interest to produce a transgenic plant or plant cell; and, optionally,
- b) regenerating a transgenic plant from said transformed plant cell.

9. The method of claim 8, further comprising producing seed from said transgenic plant and collecting said seed.

\* \* \* \* \*